

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: February 3, 2004, 04:34:02 ; Search time 1019.42 Seconds  
(without alignments)  
1025.182 Million cell updates/sec

Title: US-09-801-371A-2  
Perfect score: 43  
Sequence: 1 tcaaaactgggctccagaa.....actgggctccagctttga 43

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	248	14	T29839
2	43	100.0	474	13	BX118951
3	43	100.0	630	14	CB528492
4	43	100.0	645	14	CD370363

C	5	43	100.0	684	14	CA307429	UI-H-FTL-
C	6	43	100.0	688	14	CD367676	UI-H-FTL-
C	7	43	100.0	696	14	CA307225	UI-H-FTL-
C	8	43	100.0	699	14	CD364761	UI-H-FT2-
C	9	43	100.0	703	14	CD368142	UI-H-FTL-
C	10	43	100.0	713	14	CA308256	UI-H-FTL-
C	11	43	100.0	719	14	CB528694	UI-H-FT2-
C	12	43	100.0	722	12	BQ007008	UI-H-EI1-
C	13	43	100.0	722	14	CA307062	UI-H-FTL-
C	14	43	100.0	722	14	CD364988	UI-H-FT2-
C	15	43	100.0	723	14	CA308777	UI-H-FTL-
C	16	43	100.0	723	14	CD368116	UI-H-FTL-
C	17	43	100.0	724	14	CA309711	UI-H-FTL-
C	18	43	100.0	726	14	CA310368	UI-H-FTL-
C	19	43	100.0	726	14	CD368929	UI-H-FTL-
C	20	43	100.0	742	14	CA309509	UI-H-FTL-
C	21	43	100.0	744	14	CD366187	UI-H-FTL-
C	22	43	100.0	748	14	CA306559	UI-H-FTL-
C	23	43	100.0	1201	9	AL543083	AL543083
C	24	42	97.7	693	14	CD367625	UI-H-FTL-
C	25	41.4	96.3	672	14	CD367664	UI-H-FTL-
C	26	41.4	96.3	713	14	CA309664	UI-H-FTL-
C	27	41.4	96.3	718	14	CD367794	UI-H-FTL-
C	28	35.2	81.9	581	9	AI242177	AI242177 qh81g08.x
C	29	33.6	78.1	564	9	AA699697	AA699697 zi78fi12.s
C	30	28	65.1	561	10	BG232086	BG232086 naf32a06.
C	31	25	58.1	1011	9	AL575811	AL575811
C	32	24.8	57.7	431	28	AQ459761	AQ459761 HS 5125 A
C	33	24.6	57.2	608	14	CB426950	CB426950 602494 MA
C	34	24	55.8	594	14	N26123	N26123 vx90h08.s1
C	35	23.8	55.3	163	10	BF737938	BF737938 CM2-KT003
C	36	23.8	55.3	363	13	BY014887	BY014887 BY014887
C	37	23.6	54.9	172	10	BF855413	BF855413 RC4-FN020
C	38	23.4	54.4	434	14	CB759234	CB759234 AMGNNUC:N
C	39	23.4	54.4	492	13	BY243201	BY243201 BY243201
C	40	23.4	54.4	763	13	BQ445871	BQ445871 UI-H-EU1-
C	41	23.4	54.4	2686	11	AK077502	AK077502 Mus muscu
C	42	23.2	54.0	1025	13	BQ229625	BQ229625 AGENCOURT
C	43	23.2	54.0	1057	12	BM550588	BM550588 AGENCOURT
C	44	23	53.5	563	9	AA436782	AA436782 zv70g11.r
C	45	23	53.5	641	28	BZ158885	BZ158885 CH230-387

ALIGNMENTS

RESULT 1  
T29839  
LOCUS T29839 248 bp mRNA linear EST 06-SEP-1995  
DEFINITION EST97164 Human Testis Homo sapiens CDNA 5', end similar to tumor necrosis factor, alpha (HT:1190), mRNA sequence.  
ACCESSION T29839  
VERSION T29839.1 GI:611937  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 248)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult ,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald ,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei

Y.-F., Wing J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence

Nature 377, 3-174 (1995)

96026280

7566098

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org)

Seq primer: M13 Reverse

Location/Qualifiers

1. .248

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="ATCC (inhost):107667"

/db\_xref="taxon:9606"

/clone\_lib="Human Testis"

/note="Organ: testis"

63 a 65 c 60 g 57 t 3 others

BASE COUNT

ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 248;

Best Local Similarity 100.0%; Pred. No. 8.8e-05;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43

Db

62 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 104

RESULT 2

BX118951

LOCUS

DEFINITION BX118951 Soares fetal heart NbHL19W Homo sapiens cDNA clone

IMAGp998L124300; IMAGE:1693595, mRNA sequence.

ACCESSION

VERSION BX118951

KEYWORDS BX118951.1 GI:27882696

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 474)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,

Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

Unpublished

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998L124300.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human UnigeneSet - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTTACACAGGAAACAGCTATGAC.

FEATURES

source

1. .474

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGp998L124300 ; IMAGE:1693595"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NbHL19W"

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo (dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by

M.Fatima Bonaldo. This library was constructed from the

same fetus as the fetal lung library, Soares fetal lung

NbHL19W."

BASE COUNT 112 a 118 c 113 g 131 t

ORIGIN

Query Match 100.0%; Score 43; DB 13; Length 474;

Best Local Similarity 100.0%; Pred. No. 0.0001;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43

Db

69 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 111

RESULT 3

CB528492/c

LOCUS

DEFINITION UI-H-FT2-bjd-e-20-0-UI.s1 NCI CGAP\_FT2 Homo sapiens cDNA clone

UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.

ACCESSION

VERSION CB528492

KEYWORDS CB528492.1 GI:29388228

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 630)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 1-29, >AT-rich#Low complexity (matched complement)

205-279, >(TAAA)n#Simple\_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1. .630

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-H-FT2-bjd-e-20-0-UI"

/tissue\_type="Aveolar Macrophage"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP\_FT2"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LiB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
TAG\_137 c 139 g 174 t

Query Match 100.0%; Score 43; DB 14; Length 630;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 499 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 457

RESULT 4  
CD370363/c  
LOCUS  
DEFINITION  
UI-H-FT1-bkb-n-03-0-UI.s1 NCI CGAP\_FT1 Homo sapiens cDNA clone  
UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.  
CD370363  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/cgap.html  
The following repetitive elements were found in this cDNA  
sequence: 294-368, >(TAAA)n#simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..645  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bkb-n-03-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LiB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
TAG\_145 c 144 g 165 t

Query Match 100.0%; Score 43; DB 14; Length 645;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546

RESULT 5  
CA307429/c  
LOCUS  
DEFINITION  
UI-H-FT1-bic-i-01-0-UI.s1 NCI CGAP\_FT1 Homo sapiens cDNA clone  
UI-H-FT1-bic-i-01-0-UI 3', mRNA sequence.  
CA307429  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bent-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..684  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bic-i-01-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W.

Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 197 a 150 c 158 g 177 t 2 others  
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 684;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
|||||  
Db 591 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 549  
|||||

## RESULT 6

CD367676/c

LOCUS

DEFINITION UI-H-FT1-bjr-1-14-0-UI.s1 NCI CGAP\_FTI Homo sapiens cDNA clone  
UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.

CD367676

ACCESSION CD367676.1 GI:31151766

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 688)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 69-143, >(TAAA)n#Simple\_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..688  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bjr-1-14-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FTI"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP\_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-FT1

TAG\_TISSUE=Human Lung Aveolar Macrophage

TAG\_SEQ=GGCCATGCCG"

BASE COUNT 176 a 148 c 181 g 183 t

ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 688;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
|||||  
Db 363 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 321  
|||||

## RESULT 7

CA307225/c

LOCUS

DEFINITION UI-H-FT1-bhu-n-04-0-UI.s1 NCI CGAP\_FTI Homo sapiens cDNA clone  
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.

CA307225

ACCESSION CA307225.1 GI:24470279

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 696)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 296-370, >(TAAA)n#Simple\_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..696  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bhu-n-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FTI"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP\_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-FT1

TAG\_TISSUE=Human Lung Aveolar Macrophage

TAG\_SEQ=GGCCATGCCG"

BASE COUNT

ORIGIN

198 a 155 c 160 g 181 t 2 others



Query Match 100.0%; Score 43; DB 14; Length 696;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 590 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548

RESULT 8  
CD364761/c  
LOCUS  
DEFINITION  
UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone  
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.  
CD364761  
CD364761.1 GI:31148851  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 699)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 296-370, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1. .699  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjm-j-11-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."  
TAG\_LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
BASE COUNT 200 a 157 c 160 g 182 t  
ORIGIN  
Query Match 100.0%; Score 43; DB 14; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 590 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548

CD368142/c  
LOCUS  
DEFINITION  
UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.  
CD368142  
CD368142.1 GI:31152232  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 703)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 298-372, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
CD368142/c  
LOCUS  
DEFINITION  
UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.  
CD368142  
CD368142.1 GI:31152232  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 703)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 298-372, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Location/Qualifiers  
1. .703  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bjv-e-20-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
BASE COUNT 197 a 158 c 161 g 185 t 2 others  
ORIGIN  
Query Match 100.0%; Score 43; DB 14; Length 703;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 592 TCAAACTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 550

RESULT 10  
CA308256/c  
LOCUS  
DEFINITION  
UI-H-FT1-bhy-e-14-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bhy-e-14-0-UI 3', mRNA linear EST 01-NOV-2002

RESULT 10  
CA308256/c  
LOCUS  
DEFINITION  
UI-H-FT1-bhy-e-14-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bhy-e-14-0-UI 3', mRNA linear EST 01-NOV-2002

ACCESSION CA308256  
VERSION CA308256.1 GI:24471310  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 713)  
JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 296-370, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..713  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bhy-e-14-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI-CGAP\_FTI"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI CGAP\_FTI is a normalized cDNA library constructed from  
a pool of 81 RNA samples from Alveolar Macrophages  
challenged with different treatments. The library was  
normalized according to Bonaldo, Lennon and Soares, Genome  
Research, 6:791-806, 1996. First strand cDNA synthesis was  
primed with an oligo-dT primer containing a Not I site.  
Double stranded cDNA was ligated to an EcoR I adaptor,  
digested with Not I, and cloned directionally into  
pT7T3-Pac vector. The oligonucleotide used to prime the  
synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
GGCCATGCCG. The tissue was provided by Dr. Gary W.  
Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 164 c 161 g 184 t 1 others  
ORIGIN  
Query Match 100.0%; Score 43; DB 14; Length 713;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
DB 590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548  
|||||

RESULT 11  
CB528694/c  
LOCUS  
DEFINITION  
UI-H-FT2-bjd-1-22-0-UI.s1 NCI-CGAP\_FTI2 Homo sapiens cDNA clone  
UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.  
CB528694  
ACCESSION  
VERSION

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 719)  
JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 294-368, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..719  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjd-1-22-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI-CGAP\_FTI2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI CGAP\_FTI2 is a subtracted cDNA library constructed from  
a pool of 81 RNA samples from Alveolar Macrophages  
challenged with different treatments. The library was  
subtracted according to Bonaldo, Lennon and Soares, Genome  
Research, 6:791-806, 1996. The tissue was provided by Dr.  
Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 163 c 163 g 188 t 2 others  
ORIGIN  
Query Match 100.0%; Score 43; DB 14; Length 719;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
DB 588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546  
|||||

RESULT 12  
BQ007008/c  
LOCUS  
DEFINITION  
UI-H-E11-azb-j-22-0-UI.s1 NCI-CGAP\_E11 Homo sapiens cDNA clone  
IMAGE:5846517 3', mRNA sequence.  
BQ007008  
ACCESSION  
VERSION BQ007008.1 GI:19731908  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 722)  
JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 The following repetitive elements were found in this cDNA  
 sequence: 297-371, >(TAAA)n#Simple\_repeat  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

#### FEATURES source

Location/Qualifiers  
 1. .722  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5846517"  
 /tissue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP E11"

/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP\_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is ACACTTGCAC."

TAG\_LIB=UI-H-E11  
 TAG\_TISSUE=chondrosarcoma  
 TAG\_SEQ=ACACTTGCAC"

BASE COUNT 204 a 162 c 164 g 190 t 2 others  
 ORIGIN

Query Match 100.0%; Score 43; DB 12; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
 |||||  
 Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

#### RESULT 13 CA307062/c

LOCUS CA307062 722 bp mRNA linear EST 01-NOV-2002  
 DEFINITION UI-H-FT1-bhu-o-04-0-UI.s1 NCI CGAP\_FTI Homo sapiens cDNA clone  
 UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.

ACCESSION CA307062.1 GI:24470116  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)

SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 722)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

REFERENCE Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cgapbs-r@mail.nih.gov

TISSUE Procurement: Dr. Gary W. Hunninghake, U of I  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

The following repetitive elements were found in this cDNA

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 The following repetitive elements were found in this cDNA  
 sequence: 295-369, >(TAAA)n#Simple\_repeat  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

#### FEATURES source

Location/Qualifiers  
 1. .722  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FT1-bhu-o-04-0-UI"  
 /tissue\_type="Aveolar Macrophage"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP\_FTI"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP\_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCATGCGC. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-FT1  
 TAG\_TISSUE=Human Lung Aveolar Macrophage  
 TAG\_SEQ=GGCCATGCGC"

BASE COUNT 203 a 165 c 163 g 189 t 2 others  
 ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
 |||||  
 Db 589 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 547

#### RESULT 14 CD364988/c

LOCUS CD364988 722 bp mRNA linear EST 29-MAY-2003  
 DEFINITION UI-H-FT2-bjn-c-04-0-UI.s1 NCI CGAP\_FT2 Homo sapiens cDNA clone  
 UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.

ACCESSION CD364988  
 VERSION CD364988.1 GI:31149078  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 722)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

REFERENCE Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cgapbs-r@mail.nih.gov

TISSUE Procurement: Dr. Gary W. Hunninghake, U of I  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
 The following repetitive elements were found in this cDNA

sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..722  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjn-c-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."  
TAG\_LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 201 a 166 c 163 g 190 t 2 others  
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 591 TCAAACTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

RESULT 15  
CA308777/c

LOCUS  
DEFINITION  
UI-H-FT1-bhy-b-23-0-UI.s1 NCI\_CGAP\_FT1 Homo sapiens cDNA clone  
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
CA308777.1 GI:24471831

ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 723)

REFERENCE  
AUTHORS  
TITLE  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL

COMMENT  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bhy-b-23-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa."  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 164 c 164 g 191 t 1 others  
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 723;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 591 TCAAACTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

Search completed: February 3, 2004, 06:12:19  
Job time : 1022.42 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 05:14:03 ; Search time 764.932 Seconds  
(without alignments)  
207.072 Million cell updates/sec

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Perfect score: 43  
Sequence: 1 tcaactgggctccagaa.....actgggctacagcttga 43

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues 4899406  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	43	100.0	43	10	US-09-801-371A-6
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4	43	100.0	81	10	US-09-801-371A-7
5	43	100.0	104	10	US-09-801-371A-1
6	43	100.0	104	10	US-09-801-371A-5
7	43	100.0	1279	13	US-10-247-671-120
8	43	100.0	1643	13	US-10-310-793-9
9	43	100.0	1643	15	US-10-272-411-4
10	43	100.0	1643	15	US-10-218-547-3
11	43	100.0	1643	15	US-10-272-328A-4
12	43	100.0	1666	13	US-10-247-671-68
13	43	100.0	3634	11	US-09-824-322B-1
14	43	100.0	3634	11	US-09-932-300-34
15	43	100.0	3634	13	US-10-191-997-104

16	43	100.0	4830	12	US-10-429-802-33	Sequence 33, Appl
17	43	100.0	4830	12	US-10-430-503-24	Sequence 24, Appl
18	35	81.4	418	10	US-09-796-692-6223	Sequence 6223, Ap
19	35	81.4	418	12	US-10-057-475B-6223	Sequence 6223, Ap
20	35	81.4	418	12	US-10-154-884B-6223	Sequence 6223, Ap
21	35	81.4	418	15	US-10-040-862-6223	Sequence 6223, Ap
22	30.6	71.2	51	10	US-09-801-371A-10	Sequence 10, Appl
23	25.4	59.1	3673778	13	US-10-312-841-2	Sequence 2, Appli
24	23	53.5	260	11	US-09-535-459-1127	Sequence 1127, Ap
25	22.8	53.0	696	13	US-10-027-632-110108	Sequence 110108,
26	22.8	53.0	696	14	US-10-027-632-110108	Sequence 110108,
27	22.6	52.6	232	12	US-10-242-535A-46829	Sequence 46829, A
28	22.6	52.6	612	13	US-10-027-632-110698	Sequence 110698,
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31	22.4	52.1	922	14	US-10-027-632-120081	Sequence 120081,
32	22.2	51.6	27	10	US-09-801-371A-11	Sequence 11, Appl
33	22.2	51.6	3673778	13	US-10-312-841-1	Sequence 1, Appli
34	22	51.2	363	10	US-09-783-590-10563	Sequence 10563, A
35	21.4	49.8	406	10	US-09-560-863-146	Sequence 146, App
36	21.4	49.8	614	13	US-10-027-632-279282	Sequence 279282,
37	21.4	49.8	614	14	US-10-027-632-279282	Sequence 279282,
38	21.4	49.8	990	12	US-10-369-493-36947	Sequence 36947, A
39	21.4	49.8	1274	10	US-09-981-876-72	Sequence 72, Appl
40	21.4	49.8	1274	11	US-09-148-545-72	Sequence 72, Appl
41	21.4	49.8	1296	10	US-09-981-876-126	Sequence 126, App
42	21.4	49.8	1296	11	US-09-148-545-126	Sequence 126, App
43	21.4	49.8	1343	10	US-09-925-300-779	Sequence 779, App
44	21.4	49.8	3113	11	US-09-764-891-5580	Sequence 5580, Ap
45	21.4	49.8	4831	13	US-10-252-157-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-801-371A-2  
; Sequence 2, Application US/09801371A  
; Patent No. US20020155569A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaempfer, Raymond  
; APPLICANT: Osman, Farhat  
; APPLICANT: Jarrous, Nayef  
; APPLICANT: Ben-Asouli, Yitzhak  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH  
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES  
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147  
; CURRENT APPLICATION NUMBER: US/09/801,371A  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT WO 00/14255  
; PRIOR FILING DATE: 1999-09-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 43  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-371A-2

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RESULT 2  
US-09-801-371A-6/c  
; Sequence 6, Application US/09801371A  
; Patent No. US20020155569A1  
; GENERAL INFORMATION:

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; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

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Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

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Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
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; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

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RESULT 5
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

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Db      5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 6
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
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; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

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RESULT 7
US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 120
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

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Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
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; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-310-793-9

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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 9
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

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Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 10

US-10-218-547-3  
; Sequence 3, Application US/10218547  
; Publication No. US20030100074A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel  
; TITLE OF INVENTION: Human Endokine Alpha  
; FILE REFERENCE: PF561  
; CURRENT APPLICATION NUMBER: US/10/218,547  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/312,542  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/330,761  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: human  
US-10-218-547-3

Query Match 100.0%; Score 43; DB 15; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 11

US-10-272-328A-4  
; Sequence 4, Application US/10272328A  
; Publication No. US20030109444A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0206  
; CURRENT APPLICATION NUMBER: US/10/272,328A  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 51  
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; SEQ ID NO 4  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-272-328A-4

Query Match 100.0%; Score 43; DB 15; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 12

US-10-247-671-68  
; Sequence 68, Application US/10247671  
; Publication No. US20030194721A1  
; GENERAL INFORMATION:

; APPLICANT: Mikita, Thomas  
; APPLICANT: Shiffman, Dov  
; APPLICANT: Porter, Gordon, J.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
; FILE REFERENCE: PA-0050 US  
; CURRENT APPLICATION NUMBER: US/10/247,671  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/323,784  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PERL Program  
; SEQ ID NO 68  
; LENGTH: 1666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030194721A1 223092.1  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 1347, 1358  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-247-671-68

Query Match 100.0%; Score 43; DB 13; Length 1666;  
Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1089 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1131

RESULT 13

US-09-824-322B-1  
; Sequence 1, Application US/09824322B  
; Publication No. US20030022848A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-AL  
; TITLE OF INVENTION: ALPHA) EXPRESSION  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 1  
; LENGTH: 3634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)  
; NAME/KEY: exon  
; LOCATION: (615)..(981)  
; NAME/KEY: intron  
; LOCATION: (982)..(1588)  
; NAME/KEY: exon  
; LOCATION: (1589)..(1634)  
; NAME/KEY: intron  
; LOCATION: (1635)..(1821)  
; NAME/KEY: exon  
; LOCATION: (1822)..(1869)  
; NAME/KEY: intron  
; LOCATION: (1870)..(2070)  
; NAME/KEY: exon



LOCATION: (2171)..(3381)  
PUBLICATION INFORMATION:  
AUTHORS: Nedwin, G.E.  
AUTHORS: Naylor, S.L.  
AUTHORS: Sakaguchi, A.Y.  
AUTHORS: Smith, D.  
AUTHORS: Jarrett-Nedwin, J.  
AUTHORS: Pennica, D.  
AUTHORS: Goeddel, D.V.  
AUTHORS: Gray, P.W.  
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and  
TITLE: Chromosomal localization  
JOURNAL: Nucleic Acids Res.  
VOLUME: 13  
ISSUE: 17  
PAGES: 6361-6373  
DATE: 1985-09-11  
DATABASE ACCESSION NUMBER: X02910 Genbank  
DATABASE ENTRY DATE: 1997-02-17  
US-09-824-322B-1

Query Match 100.0%; Score 43; DB 11; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

## RESULT 14

US-09-932-300-34  
Sequence 34, Application US/09932300  
Publication No. US20030032788A1

GENERAL INFORMATION:  
APPLICANT: GARVER, Eric  
APPLICANT: TU, Guang-Chou  
APPLICANT: ISRAEL, Yedy  
TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION  
FILE REFERENCE: 9855-302  
CURRENT APPLICATION NUMBER: US/09/932,300  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: US 60/051,705  
PRIOR FILING DATE: 1997-07-03  
PRIOR APPLICATION NUMBER: US 09/109,663  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 111  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 34  
LENGTH: 3634  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-932-300-34

Query Match 100.0%; Score 43; DB 11; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

## RESULT 15

US-10-191-997-104  
Sequence 104, Application US/10191997  
Publication No. US20030207834A1

GENERAL INFORMATION:  
APPLICANT: Oligos Etc., Inc.  
APPLICANT: DALE, Roderic M. K.  
APPLICANT: ARROW, Amy  
APPLICANT: THOMPSON, Terry  
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their

FILE REFERENCE: 54800-5019  
CURRENT APPLICATION NUMBER: US/10/191,997  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US 60/303,820  
PRIOR FILING DATE: 2001-07-10  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 104  
LENGTH: 3634  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: X02910  
US-10-191-997-104

Query Match 100.0%; Score 43; DB 13; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

Search completed: February 3, 2004, 09:06:06  
Job time : 770.932 secs

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OM nucleic - nucleic search, using sw model  
Run on: February 3, 2004, 04:34:26 ; Search time 33.3469 Seconds  
(without alignments)  
569.152 Million cell updates/sec

Title: US-09-801-371A-2  
Perfect score: 43  
Sequence: 1 tcaaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	787	4	US-09-032-297A-13
2	43	100.0	787	4	US-09-229-151C-7
3	43	100.0	1643	3	US-08-880-342-36
4	43	100.0	1643	4	US-09-505-250-4
5	43	100.0	2270	4	US-09-229-151C-13
6	43	100.0	2570	4	US-09-229-151C-14
7	43	100.0	3634	3	US-09-166-186-1
8	43	100.0	3634	3	US-09-313-932-1
9	43	100.0	3634	3	US-09-109-663-34
10	21.4	49.8	24707	4	US-09-740-027-3
11	21	48.8	771	5	PCT-US95-12987-1
12	21	48.8	771	5	PCT-US95-12987-3
13	21	48.8	771	5	PCT-US95-12987-5
14	20.8	48.4	861	1	US-08-409-731A-1
15	20.8	48.4	861	2	US-08-470-298B-1
16	20.8	48.4	861	2	US-09-023-073A-1
17	20.8	48.4	861	3	US-09-361-737-1
18	20.8	48.4	944	2	US-08-820-825-1
19	20.8	48.4	944	3	US-09-307-817-1
20	20.8	48.4	944	4	US-09-734-036-1
21	20.8	48.4	957	3	US-08-899-031-2
22	20.8	48.4	65042	4	US-09-784-316-3
23	20	46.5	20	3	US-09-166-186-32
24	20	46.5	20	3	US-09-166-186-212
25	20	46.5	20	3	US-09-166-186-213
26	20	46.5	20	3	US-09-166-186-214
27	20	46.5	20	3	US-09-313-932-32

C 28	20	46.5	20	3	US-09-313-932-212	Sequence 212, App
C 29	20	46.5	20	3	US-09-313-932-213	Sequence 213, App
C 30	20	46.5	20	3	US-09-313-932-214	Sequence 214, App
C 31	20	46.5	20	3	US-09-313-932-354	Sequence 354, App
C 32	20	46.5	20	3	US-09-313-932-357	Sequence 357, App
C 33	20	46.5	20	3	US-09-313-932-358	Sequence 358, App
C 34	20	46.5	20	3	US-09-313-932-361	Sequence 361, App
C 35	20	46.5	20	3	US-09-313-932-468	Sequence 468, App
C 36	19.8	46.0	3431	4	US-09-632-098-1	Sequence 1, Appli
C 37	19.8	46.0	3468	4	US-09-632-098-3	Sequence 3, Appli
C 38	19.8	46.0	4695	2	US-08-231-193A-57	Sequence 57, Appl
C 39	19.8	46.0	4695	2	US-08-486-273A-57	Sequence 57, Appl
C 40	19.8	46.0	4695	3	US-08-940-086A-57	Sequence 57, Appl
C 41	19.8	46.0	4695	4	US-08-940-035A-57	Sequence 57, Appl
C 42	19.8	46.0	4695	4	US-08-935-105A-57	Sequence 57, Appl
C 43	19.8	46.0	4695	4	US-09-648-797-57	Sequence 57, Appl
C 44	19.8	46.0	4695	4	US-09-386-123-57	Sequence 57, Appl
C 45	19.4	45.1	298	4	US-09-313-294A-5776	Sequence 5776, Ap

ALIGNMENTS

RESULT 1  
US-09-032-297A-13  
; Sequence 13, Application US/09032297A  
; Patent No. 6525184  
; GENERAL INFORMATION:  
; APPLICANT: Revati J. Tataka, Steven D. Marlin and  
; Randall W. Barton  
; TITLE OF INVENTION: Self-Regulated Apoptosis of  
; Inflammatory Cells by Gene Therapy  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Boehringer Ingelheim Corporation  
; STREET: 900 Ridgebury Road, P.O. Box 368  
; CITY: Ridgefield  
; STATE: Connecticut  
; COUNTRY: United States of America  
; ZIP: 06877-0368  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Processing  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,297A  
; FILING DATE: 27-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,266  
; FILING DATE: 28-FEB-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robert P. Raymond  
; REGISTRATION NUMBER: 25089  
; REFERENCE/DOCKET NUMBER: 9/121PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203-791-6183  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 787  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: <Unknown>  
; DESCRIPTION: DNA  
; FEATURE:  
; NAME/KEY: TNFa 3' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-032-297A-13

Query Match 100.0%; Score 43; DB 4; Length 787;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 226 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 268

RESULT 2  
US-09-229-151C-7  
; Sequence 7, Application US/09229151C  
; Patent No. 6537784  
; GENERAL INFORMATION:  
; APPLICANT: Tatake, Revati J.  
; APPLICANT: Marlin, Steven D.  
; APPLICANT: Barton, Randall W.  
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy  
; FILE REFERENCE: 9/137  
; CURRENT APPLICATION NUMBER: US/09/229,151C  
; CURRENT FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: US 60/076,316  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 7  
; LENGTH: 787  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; OTHER INFORMATION: TNF-alpha untranslated region  
US-09-229-151C-7

Query Match 100.0%; Score 43; DB 4; Length 787;  
Best Local Similarity 100.0%; Pred. No. 1.5e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 226 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 268

RESULT 3  
US-08-880-342-36  
; Sequence 36, Application US/08880342  
; Patent No. 6218179  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; APPLICANT: Murphy, Brian  
; APPLICANT: Laderoute, Keith R.  
; APPLICANT: Green, Christopher J.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,342  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB95/00996  
; FILING DATE: 13-NOV-1995  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/365,486  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1643 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: TNF CDNA HSTNFR (EMBL Accession  
; INDIVIDUAL ISOLATE: #X01394)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 153..851  
US-08-880-342-36

Query Match 100.0%; Score 43; DB 3; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 1074 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1116

RESULT 4  
US-09-505-250-4  
; Sequence 4, Application US/09505250A  
; Patent No. 6329148  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Glenn  
; APPLICANT: Kao, Peter  
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with  
; TITLE OF INVENTION: Triptolides and Death Domain Ligands  
; FILE REFERENCE: SUN-109PRV2  
; CURRENT APPLICATION NUMBER: US/09/505,250A  
; CURRENT FILING DATE: 2000-02-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (153)...(854)  
US-09-505-250-4

Query Match 100.0%; Score 43; DB 4; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 1074 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1116

RESULT 5  
US-09-229-151C-13  
; Sequence 13, Application US/09229151C  
; Patent No. 6537784  
; GENERAL INFORMATION:  
; APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.  
APPLICANT: Barton, Randall W.  
TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy  
FILE REFERENCE: 9/137  
CURRENT APPLICATION NUMBER: US/09/229,151C  
CURRENT FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: US 60/076,316  
PRIOR FILING DATE: 1998-02-27  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 2.0  
SEQ ID NO 13  
LENGTH: 2270  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR  
US-09-229-151C-13

Query Match 100.0%; Score 43; DB 4; Length 2270;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1751

## RESULT 6

US-09-229-151C-14  
Sequence 14, Application US/09229151C  
Patent No. 6537784

## GENERAL INFORMATION:

APPLICANT: Tataka, Revati J.  
APPLICANT: Marlin, Steven D.  
APPLICANT: Barton, Randall W.  
TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy  
FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: US 60/076,316

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 2.0

SEQ ID NO 14

LENGTH: 2570

TYPE: DNA

ORGANISM: Human

FEATURE:

OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR

US-09-229-151C-14

Query Match 100.0%; Score 43; DB 4; Length 2570;  
Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051

## RESULT 7

US-09-166-186-1  
Sequence 1, Application US/09166186A  
Patent No. 6080580

## GENERAL INFORMATION:

APPLICANT: Baker, Brenda  
APPLICANT: Bennett, C. Frank  
APPLICANT: Butler, Madeline M.  
APPLICANT: Shanahan, William R.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$  EXPRESSION  
FILE REFERENCE: ISPH-0322  
CURRENT APPLICATION NUMBER: US/09/166,186A  
CURRENT FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 250  
SEQ ID NO 1  
LENGTH: 3634  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (615)..(981)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (982)..(1588)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1589)..(1634)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (1635)..(1821)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1822)..(1869)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (1870)..(2070)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (2171)..(3381)  
PUBLICATION INFORMATION:  
AUTHORS: Nedwin, G.E.  
AUTHORS: Naylor, S.L.  
AUTHORS: Sakaguchi, A.Y.  
AUTHORS: Smith, D.  
AUTHORS: Jarrett-Nedwin, J.  
AUTHORS: Pennica, D.  
AUTHORS: Goeddel, D.V.  
AUTHORS: Gray, P.W.  
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,  
TITLE: homology and chromosomal localization  
JOURNAL: Nucleic Acids Res.  
VOLUME: 13  
ISSUE: 17  
PAGES: 6361-6373  
DATE: 1985-09-11  
DATABASE ACCESSION NUMBER: X02910 Genbank  
DATABASE ENTRY DATE: 1997-02-17  
US-09-166-186-1

Query Match 100.0%; Score 43; DB 3; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

## RESULT 8

US-09-313-932-1  
Sequence 1, Application US/09313932A  
Patent No. 6228642

## GENERAL INFORMATION:

APPLICANT: Baker, Brenda  
APPLICANT: Bennett, C. Frank  
APPLICANT: Butler, Madeline M.  
APPLICANT: Shanahan, William R.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$   
FILE REFERENCE: ISPH-0356  
CURRENT APPLICATION NUMBER: US/09/313,932A  
CURRENT FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 501



SEQ ID NO 1  
LENGTH: 3634  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (615)..(981)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (982)..(1588)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1589)..(1634)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (1635)..(1821)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (1822)..(1869)  
FEATURE:  
NAME/KEY: intron  
LOCATION: (1870)..(2070)  
FEATURE:  
NAME/KEY: exon  
LOCATION: (2171)..(3381)  
PUBLICATION INFORMATION:  
AUTHORS: Nedwin, G.E.  
AUTHORS: Naylor, S.L.  
AUTHORS: Sakaguchi, A.Y.  
AUTHORS: Smith, D.  
AUTHORS: Jarrett-Nedwin, J.  
AUTHORS: Pennica, D.  
AUTHORS: Goeddel, D.V.  
AUTHORS: Gray, P.W.  
TITLE: Human lymphotoxin and tumor necrosis factor genes:  
TITLE: structure, homology and chromosomal localization  
JOURNAL: Nucleic Acids Res.  
VOLUME: 13  
ISSUE: 17  
PAGES: 6361-6373  
DATE: 1985-09-11  
DATABASE ACCESSION NUMBER: X02910 Genbank  
DATABASE ENTRY DATE: 1997-02-17  
US-09-313-932-1

Query Match 100.0%; Score 43; DB 3; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 2854

RESULT 9  
US-09-109-663-34  
Sequence 34, Application US/09109663  
Patent No. 6277981  
GENERAL INFORMATION:  
APPLICANT: Tu, Guang-Chou  
APPLICANT: Israel, Yedy  
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF  
TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES  
FILE REFERENCE: 9855-3U1  
CURRENT APPLICATION NUMBER: US/09/109,663  
CURRENT FILING DATE: 1998-07-03  
EARLIER APPLICATION NUMBER: 60/051,705  
EARLIER FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 34  
LENGTH: 3634  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: TNF(alpha) cDNA  
US-09-109-663-34

Query Match 100.0%; Score 43; DB 3; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGA 2854

RESULT 10

US-09-740-027-3  
Sequence 3, Application US/09740027  
Patent No. 6485939

GENERAL INFORMATION:

APPLICANT: YE, Jane et al  
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR  
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER  
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF  
FILE REFERENCE: CL001052  
CURRENT APPLICATION NUMBER: US/09/740,027  
CURRENT FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 24707

TYPE: DNA

ORGANISM: Human

US-09-740-027-3

Query Match 49.8%; Score 21.4; DB 4; Length 24707;  
Best Local Similarity 80.6%; Pred. No. 16;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGC 31  
Db 11941 TCCACATTGCCCTCCGGAACCTCACTGGGGC 11971

RESULT 11

PCT-US95-12987-1  
Sequence 1, Application PC/TUS9512987  
GENERAL INFORMATION:

APPLICANT: LAFEMINA, R.  
APPLICANT: SARDANA, V.  
APPLICANT: VELOSKI, C.  
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: ROY D. MEREDITH  
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/12987  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MEREDITH, ROY D.

REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 19262 PCT  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 771 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-12987-1

Query Match 48.8%; Score 21; DB 5; Length 771;  
Best Local Similarity 73.0%; Pred. No. 13;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAG 37  
DB 539 TCACACAGCGGTTTCCAGACCTCAGCGGCGCGACCG 575

## RESULT 12

PCT-US95-12987-3  
Sequence 3, Application PC/TUS9512987  
GENERAL INFORMATION:

APPLICANT: LAFEMINA, R.  
APPLICANT: SARDANA, V.  
APPLICANT: VELOSKI, C.  
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: ROY D. MEREDITH  
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.  
CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/12987

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MEREDITH, ROY D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: 19262 PCT

TELEPHONE: (908) 594-4678

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 771 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US95-12987-3

Query Match 48.8%; Score 21; DB 5; Length 771;  
Best Local Similarity 73.0%; Pred. No. 13;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAG 37  
DB 539 TCACACAGCGGTTTCCAGACCTCAGCGGCGCGACCG 575

## RESULT 13

PCT-US95-12987-5  
Sequence 5, Application PC/TUS9512987  
GENERAL INFORMATION:

APPLICANT: LAFEMINA, R.

APPLICANT: SARDANA, V.

APPLICANT: VELOSKI, C.

TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROY D. MEREDITH

STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/12987

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MEREDITH, ROY D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: 19262 PCT

TELEPHONE: (908) 594-4678

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 771 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US95-12987-5

Query Match 48.8%; Score 21; DB 5; Length 771;  
Best Local Similarity 73.0%; Pred. No. 13;  
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAG 37  
DB 539 TCACACAGCGGTTTCCAGACCTCAGCGGCGCGACCG 575

## RESULT 14

US-08-409-731A-1  
Sequence 1, Application US/08409731A  
Patent No. 5658758

GENERAL INFORMATION:

APPLICANT: NI, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Gentz, Reiner

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: YU, GUO-LIANG  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Robert H  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PF175  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 861 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 94..414  
US-08-409-731A-1

Query Match 48.4%; Score 20.8; DB 1; Length 861;  
Best Local Similarity 78.1%; Pred. No. 16;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42  
Db 96 GCCTCCCAACCTCACTGGGCTACTACCGCTTTG 127

RESULT 15  
US-08-470-298B-1  
Sequence 1, Application US/08470298B  
Patent No. 5844081  
GENERAL INFORMATION:  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: YU, GUO-LIANG  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: CYTOSTATIN I  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,298B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ALLAN A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF175D1  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8512  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 861 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 94..414  
US-08-470-298B-1  
Query Match 48.4%; Score 20.8; DB 2; Length 861;  
Best Local Similarity 78.1%; Pred. No. 16;  
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42  
Db 96 GCCTCCCAACCTCACTGGGCTACTACCGCTTTG 127  
Search completed: February 3, 2004, 06:14:28  
Job time : 35.3469 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 03:10:21 ; Search time 119.054 Seconds  
(without alignments)  
974.981 Million cell updates/sec

Title: US-09-801-371A-2  
Perfect score: 43  
Sequence: 1 tcaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*  
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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
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24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	21	AAZ99817
2	43	100.0	50	21	AAZ99815
3	43	100.0	104	21	AAZ99816
4	43	100.0	787	20	AAZ20979
5	43	100.0	815	8	AAZ70075
6	43	100.0	817	11	AAQ04340
7	43	100.0	818	10	AAZ91035
8	43	100.0	1200	8	AAZ70072

9	43	100.0	1200	10	AAZ90969	Part of gene for a
10	43	100.0	1275	7	AAZ60558	Sequence encoding
11	43	100.0	1323	7	AAZ60363	Sequence encoding
12	43	100.0	1324	21	AAZ21085	Human low adenosin
13	43	100.0	1324	21	AAZ34963	Human adenosine re
14	43	100.0	1560	9	AAZ80219	Sequence of pE4 en
15	43	100.0	1585	7	AAZ60557	Sequence encoding
16	43	100.0	1585	7	AAZ60527	Sequence encoding
17	43	100.0	1606	7	AAZ60446	Sequence encoding
18	43	100.0	1606	17	AAZ15424	Human tumour necro
19	43	100.0	1643	8	AAZ71307	Sequence encoding
20	43	100.0	1643	17	AAZ31021	Human tumour necro
21	43	100.0	1643	24	ABK13195	Human tumour necro
22	43	100.0	1643	25	AAZ49644	Human tumour necro
23	43	100.0	1643	25	AAZ53712	Tumour necrosis fa
24	43	100.0	2270	20	AAZ20983	Chimeric nucleic a
25	43	100.0	2570	20	AAZ20984	Chimeric nucleic a
26	43	100.0	3634	19	AAZ39005	TNF-alpha gene use
27	43	100.0	3634	20	AAZ09014	Tumour necrosis fa
28	43	100.0	3634	21	AAZ63770	Human TNF-alpha ge
29	43	100.0	3634	21	AAZ40760	Human tumour necro
30	43	100.0	6911	24	AAZ45858	Human tumour necro
31	43	100.0	6911	24	AAZ45898	Human tumour necro
32	43	100.0	7112	22	AAZ6085	Lymphotoxin and tu
33	43	100.0	7112	22	AAZ57450	Human tumour necro
34	43	100.0	7112	25	AAZ51863	Human tumour necro
35	43	100.0	16310	21	AAZ21086	Human low adenosin
36	43	100.0	16310	21	AAZ34964	Human adenosine re
37	43	100.0	17634	21	AAZ21087	Human low adenosin
38	43	100.0	17634	21	AAZ21087	Human low adenosin
39	43	100.0	17634	21	AAZ34965	Human adenosine re
40	43	100.0	17634	21	AAZ34965	Human adenosine re
41	43	100.0	81800	24	ABK84756	Human CDNA differe
42	41.4	96.3	1585	15	AAZ58037	Tumour necrosis fac
43	30.6	71.2	51	21	AAZ99916	Sequence of the st
44	24.6	57.2	811	13	AAZ22830	Sequence encoding
45	24.6	57.2	1678	13	AAZ22829	Sequence encoding

ALIGNMENTS

RESULT 1  
AAZ99817  
ID AAZ99817 standard; RNA; 43 BP.

XX AAZ99817;

XX 12-JUL-2000 (first entry)

XX Cis-acting nucleotide sequence derived from human TNF-alpha.

XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;  
RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;  
tumour necrosis factor alpha; TNF-alpha; gene therapy; ss

XX Homo sapiens.

XX WO200014255-A1.

XX 16-MAR-2000.

XX 06-SEP-1999; 99WO-IL00483.

XX 07-SEP-1998; 98IL-0126112.

XX 26-OCT-1998; 98IL-0126757.

XX (YISS ) YISSUM RES & DEV CO.

XX Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX WPI; 2000-257000/22.



PT Regulation of gene expression by mRNA splicing is carried out using a  
PT cis-acting nucleotide sequence controlled by phosphorylation of the  
PT alpha-subunit of eukaryotic initiation factor 2  
XX  
PS Claim 5; Page 15; 75pp; English.

XX The specification describes a cis-acting nucleotide sequence which is  
CC capable of removing introns from a precursor transcript encoded by a  
CC gene which harbours at least one cis-acting nucleotide sequence. This  
CC removal is effected during the production of mRNA of the gene, and  
CC depends on activation of a trans-acting factor which is an RNA-activated  
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic  
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide  
CC sequence, derived from the 3' untranslated region (3'UTR) of the human  
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders  
CC splicing of precursor transcripts encoded by that gene sensitive to the  
CC level of RNA-activated protein kinase (PKR) activity. The sequence can  
CC be used to transform host cells to regulate gene expression at the mRNA  
CC splicing level, for gene therapy, and to produce a recombinant  
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural  
CC protein) or industrially or agriculturally applicable protein. The  
CC present sequence represents a cis-acting nucleotide sequence of the  
CC invention.

XX Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43

RESULT 2  
AAZ99815  
ID AAZ99815 standard; RNA; 50 BP.

XX AAZ99815;

DT 12-JUL-2000 (first entry)

DE Sequence of the stem loop of tumour necrosis factor-alpha gene.

XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;  
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;  
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

XX Homo sapiens.

OS WO200014255-A1.

PN 16-MAR-2000.

PD 06-SEP-1999; 99WO-IL00483.

XX 07-SEP-1998; 98IL-0126112.

PR 26-OCT-1998; 98IL-0126757.

XX (YISS ) YISSUM RES & DEV CO.

PA Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

PI WPI; 2000-257000/22.

XX Regulation of gene expression by mRNA splicing is carried out using a  
PT cis-acting nucleotide sequence controlled by phosphorylation of the  
PT alpha-subunit of eukaryotic initiation factor 2

XX Example 7; Fig 5B; 75pp; English.

XX The specification describes a cis-acting nucleotide sequence which is

CC capable of removing introns from a precursor transcript encoded by a  
CC gene which harbours at least one cis-acting nucleotide sequence. This  
CC removal is effected during the production of mRNA of the gene, and  
CC depends on activation of a trans-acting factor which is an RNA-activated  
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic  
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide  
CC sequence, derived from the 3' untranslated region (3'UTR) of the human  
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders  
CC splicing of precursor transcripts encoded by that gene sensitive to the  
CC level of RNA-activated protein kinase (PKR) activity. The sequence can  
CC be used to transform host cells to regulate gene expression at the mRNA  
CC splicing level, for gene therapy, and to produce a recombinant  
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural  
CC protein) or industrially or agriculturally applicable protein. The  
CC present sequence represents a fragment of the 3'UTR of human TNF-alpha.

SQ Sequence 50 BP; 12 A; 15 C; 12 G; 11 U; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 50;  
Best Local Similarity 79.1%; Pred. No. 2e-07;  
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43  
Db 5 UCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 47

RESULT 3  
AAZ99816  
ID AAZ99816 standard; RNA; 104 BP.

XX AAZ99816;

DT 12-JUL-2000 (first entry)

XX Cis-acting nucleotide sequence derived from human TNF-alpha.

XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;  
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;  
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

XX Homo sapiens.

OS WO200014255-A1.

PN 16-MAR-2000.

PD 06-SEP-1999; 99WO-IL00483.

XX 07-SEP-1998; 98IL-0126112.

PR 26-OCT-1998; 98IL-0126757.

XX (YISS ) YISSUM RES & DEV CO.

PA Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

PI WPI; 2000-257000/22.

XX Regulation of gene expression by mRNA splicing is carried out using a  
PT cis-acting nucleotide sequence controlled by phosphorylation of the  
PT alpha-subunit of eukaryotic initiation factor 2

PS Claim 4; Page 15; 75pp; English.

XX The specification describes a cis-acting nucleotide sequence which is  
CC capable of removing introns from a precursor transcript encoded by a  
CC gene which harbours at least one cis-acting nucleotide sequence. This  
CC removal is effected during the production of mRNA of the gene, and  
CC depends on activation of a trans-acting factor which is an RNA-activated  
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic  
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide  
CC sequence, derived from the 3' untranslated region (3'UTR) of the human  
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

CC splicing of precursor transcripts encoded by that gene sensitive to the  
CC level of RNA-activated protein kinase (PKR) activity. The sequence can  
CC be used to transform host cells to regulate gene expression at the mRNA  
CC splicing level, for gene therapy, and to produce a recombinant  
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural  
CC protein) or industrially or agriculturally applicable protein. The  
CC present sequence represents a cis-acting nucleotide sequence of the  
CC invention.  
XX  
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;  
Query Match 100.0%; Score 43; DB 21; Length 104;  
Best Local Similarity 100.0%; Pred. No. 2.2e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47  
RESULT 4  
ID AAZ20979 standard; DNA; 787 BP..  
XX AAZ20979;  
AC AAZ20979;  
XX 30-NOV-1999 (first entry)  
DT Human TNFalpha 3'UTR.  
DE  
XX TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;  
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;  
KW psoriasis; graft versus host disease; lupus erythematosus;  
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.  
XX  
OS Homo sapiens.  
XX WO9943840-A1.  
PN  
XX 02-SEP-1999.  
PD  
XX 12-JAN-1999; 99WO-US00637.  
PF  
XX 27-FEB-1998; 98US-0076316.  
PR  
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
PA  
XX Tatake RJ, Marlin SD, Barton RW;  
PI  
XX WPI; 1999-527630/44.  
DR  
XX  
XX A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)  
PT promoter and an apoptosis-inducing Granzyme B polynucleotide -  
PT  
XX Example 1; Page 60-61; 71pp; English.  
PS  
XX This sequence represents a human TNFalpha (tumour necrosis factor alpha)  
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)  
CC were constructed comprising at least one TNFalpha promoter enhancer  
CC region (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA  
CC encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a  
CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of  
CC cytokines produced by inflammatory cells. Upregulation and/or  
CC dysregulation of cytokines in inflamed tissue may be directly or  
CC indirectly responsible for exacerbation of chronic inflammatory  
CC diseases. Introduction of the chimeric nucleotide to activated  
CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical  
CC compositions of the chimeric nucleotide may be useful for treating  
CC inflammatory disorders such as multiple sclerosis, Crohn's disease,  
CC ulcerative colitis, psoriasis, graft versus host disease, lupus  
CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing  
CC spondylitis, and in particular, rheumatoid arthritis. The use of such  
CC chimeric nucleotides offers simpler and cheaper long-term relief, in

CC comparison with existing conventional pharmaceutical and invasive surgery  
CC methods.  
XX  
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;  
Query Match 100.0%; Score 43; DB 20; Length 787;  
Best Local Similarity 100.0%; Pred. No. 3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268  
RESULT 5  
ID AAN70075 standard; DNA; 815 BP.  
XX AAN70075;  
AC AAN70075;  
XX 25-MAR-2003 (updated)  
DT 20-JAN-1991 (first entry)  
XX Human anti-tumor polypeptide Xho-PstI fragment.  
DE  
XX Anti-tumor; cancer; cytotoxic; ss.  
KW  
XX Homo sapiens.  
OS  
XX EP247906-A.  
PN  
XX 02-DEC-1987.  
PD  
XX 04-FEB-1987; 87EP-0400261.  
PF  
XX 04-FEB-1986; 86JP-0021302.  
PR 07-FEB-1986; 86JP-0024220.  
PR 17-JUL-1986; 86JP-0169522.  
XX  
PA (MIZU/) MIZUNO D.  
XX  
XX Mizuno D;  
PI Soma GI;  
XX  
XX WPI; 1987-336540/48.  
DR  
XX Anti-tumor polypeptides - prepared using recombinant DNA prepared  
PT from genomic DNA of human acute leukemia cell THP-1.  
PT  
XX Disclosure; Fig 7; 63pp; English.  
PS  
XX The sequence is an Xho-PstI fragment of an anti-tumor protein.  
CC The polypeptide is cytotoxic to human tumor cells but not to normal  
CC cells. They are also cytotoxic to primary cell cultures obtained  
CC from metastasis lesions of patients suffering from striated muscle  
CC tumors. They are also resistant to all chemotherapeutic agents.  
CC See also AAN70073-74, AAP70077-78 and AAP95592.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 other;  
Query Match 100.0%; Score 43; DB 8; Length 815;  
Best Local Similarity 100.0%; Pred. No. 3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758  
RESULT 6  
AAQ04340  
ID AAQ04340 standard; DNA; 817 BP.

XX AAQ04340;  
AC  
XX  
DT 25-MAR-2003 (updated)  
DT 21-SEP-1990 (first entry)  
XX  
DE THP-1.  
XX  
KW Acute leukaemia cell; THP-1; anti-tumour agent; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP02088598-A.  
XX  
PD 28-MAR-1990.  
XX  
PF 22-SEP-1988; 88JP-0239154.  
XX  
PR 22-SEP-1988; 88JP-0239154.  
XX  
PA (SOMA/) SOMA G.  
XX  
DR WPI; 1990-143138/19.  
XX  
XX Intrinsic TNF prodn. derivation agents - contain primer and trigger,  
PT at least one of which has TNF activity.  
PT  
XX  
PS Disclosure; Page ?; ?pp; Japanese.  
XX  
XX Used in the prodn. of TNF prodn. agents.  
CC (Updated on 25-MAR-2003 to correct PD field.)  
CC  
XX  
SQ Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 11; Length 817;  
Best Local Similarity 100.0%; Pred. No. 3e-07; Indels 0; Gaps 0;  
Matches 43; Conservative 0; Mismatches 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758  
  
RESULT 7  
AAN91035  
ID AAN91035 standard; DNA; 818 BP.  
XX  
AC AAN91035;  
XX  
DT 11-MAR-1990 (first entry)  
XX  
DE XhoI - PstI section of gene for anti-cancer peptide.  
XX  
KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.  
XX  
OS THP-1 cells.  
XX  
PN JP01095784-A.  
XX  
PD 13-APR-1989.  
XX  
PF 06-OCT-1987; 87JP-0252174.  
XX  
PR 06-OCT-1987; 87JP-0252174.  
XX  
PA (SENG/) SEN G.  
XX  
DR WPI; 1989-154899/21.  
XX  
XX Novel DNA, plasmid and polypeptide(s)  
PT - useful as anticarcinogenic agents  
XX  
PS Fig 3; Page ?; 17pp; Japanese.

XX Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA  
CC from THP-1 cells.  
XX  
SQ Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 10; Length 818;  
Best Local Similarity 100.0%; Pred. No. 3e-07; Indels 0; Gaps 0;  
Matches 43; Conservative 0; Mismatches 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 717 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 759  
  
RESULT 8  
AAN70072  
ID AAN70072 standard; DNA; 1200 BP.  
XX  
AC AAN70072;  
XX  
DT 25-MAR-2003 (updated)  
DT 20-JAN-1991 (first entry)  
XX  
DE Human anti-tumor polypeptide.  
XX  
KW Anti-tumor; cancer; cytotoxic; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP247906-A.  
XX  
PD 02-DEC-1987.  
XX  
PF 04-FEB-1987; 87EP-0400261.  
XX  
PR 04-FEB-1986; 86JP-0021302.  
PR 07-FEB-1986; 86JP-0024220.  
PR 17-JUL-1986; 86JP-0169522.  
XX  
PA (MIZU/) MIZUNO D.  
XX  
PI Mizuno D;  
PI Soma GI;  
XX  
DR WPI; 1987-336540/48.  
XX  
PT Anti-tumor polypeptides - prepared using recombinant DNA prepared  
PT from genomic DNA of human acute leukemia cell THP-1.  
XX  
PS Disclosure; Fig 4; 63pp; English.  
XX  
CC The polypeptide is cytotoxic to human tumor cells but not to normal  
CC cells. They are also cytotoxic to primary cell cultures obtained  
CC from metastasis lesions of patients suffering from striated muscle  
CC tumors. They are also resistant to all chemotherapeutic agents.  
CC See also AAN70073-75, AAP70077-78 and AAP95592.  
CC (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 8; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07; Indels 0; Gaps 0;  
Matches 43; Conservative 0; Mismatches 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141  
  
RESULT 9  
AAN90969  
ID AAN90969 standard; DNA; 1200 BP.

XX AAN90969;  
AC  
XX  
DT 25-MAR-2003 (updated)  
DT 11-MAR-1990 (first entry)  
XX  
XX Part of gene for anti-cancer peptide.  
XX  
KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.  
XX  
XX THP-1 cells.  
PN JP01095784-A.  
XX  
PD 13-APR-1989.  
XX  
PF 06-OCT-1987; 87JP-0252174.  
XX  
PR 06-OCT-1987; 87JP-0252174.  
XX  
PA (SENG/) SEN G.  
XX  
DR WPI; 1989-154899/21.  
XX  
XX Novel DNA, plasmid and polypeptide(s)  
PT - useful as anticarcinogenic agents  
XX  
PS Fig 2; Page ?; 17pp; Japanese.  
XX  
CC Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1  
CC cells.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;

Query Match 100.0%; Score 43; DB 10; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141

RESULT 10  
AAN60558  
ID AAN60558 standard; DNA; 1275 BP.  
XX  
AC AAN60558;  
XX  
DT 28-JUL-1991 (first entry)  
XX  
DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein  
DE Ser 69 in pAW731.  
XX  
KW Antitumour; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..474  
FT /\*tag= a  
XX  
PN WO8604606-A.  
XX  
PD 14-AUG-1986.  
XX  
PF 03-FEB-1986; 86WO-US00236.  
XX  
PR 07-FEB-1985; 85US-0698939.  
PR 19-OCT-1982; 82US-0435154.  
PR 15-APR-1983; 83US-0486162.  
PR 20-DEC-1983; 83US-0564224.

PR 15-OCT-1984; 84US-0661026.  
PR 07-FEB-1985; 85US-0695934.  
XX  
PA (CETU ) CETUS CORP.  
XX  
PI Mark DF, Lin LS, Lu SDY, Wang AM;  
XX  
DR WPI; 1986-225458/34.  
DR P-PSDB; AAP60656.  
XX  
PT New synthetic muteins of human tumour necrosis factor protein -  
PT are obtd. by direct mutagenesis and retain antitumour activity  
XX  
PS Disclosure; Fig 3a; 47pp; English.  
XX  
CC The sequence encoding TNF produced by the promyelocytic leukemia  
CC cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in  
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in  
CC the TNF sequence appears to be involved in disulphide linkages. The  
CC patentors claim a novel synthetic mutein of a biologically active  
CC hTNF protein, having at least one cysteine residue free from a  
CC disulphide link and non-essential to the activity and having at  
CC least one of the cysteine residues deleted or replaced by another AA.  
CC Plasmid pAW731 (Ser 69) is claimed.  
XX  
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1275;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739

RESULT 11  
AAN60363  
ID AAN60363 standard; DNA; 1323 BP.  
XX  
AC AAN60363;  
XX  
DT 19-JUN-1991 (first entry)  
XX  
DE Sequence encoding human tumour necrosis factor.  
XX  
KW hTNF; tumour; cancer; interferon; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..534  
FT /\*tag= a  
FT sig\_peptide 1..60  
FT /\*tag= b  
FT /\*label= Secretory leader peptide  
FT mat\_peptide 61..534  
FT /\*tag= c  
XX  
PN EPI68214-A.  
XX  
PD 15-JAN-1986.  
XX  
PF 03-JUL-1985; 85EP-0304758.  
XX  
PR 03-DEC-1984; 84US-0677454.  
PR 05-JUL-1984; 84US-0627959.  
PR 05-JUL-1984; 84US-0628059.  
PR 05-JUL-1984; 84US-0628060.  
PR 03-DEC-1984; 84US-0677156.  
PR 03-DEC-1984; 84US-0677257.  
PR 25-JUL-1984; 84US-0627969.  
PR 03-DEC-1984; 84US-0677267.



XX (GETH ) GENENTECH INC.  
XX PA Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;  
XX PI WPI; 1986-015483/03.  
XX DR P-PSDB; AAF60417.  
XX PT Pure tumour necrosis factor and mutant forms - new DNA coding  
XX PT sequences and transformed cells.  
XX PS Claim 20; Fig 10; 90pp; English.  
XX CC Sequence encodes the pure human tumour necrosis factor, mutants of  
XX CC which are covered by the claims. TNF and mutants are useful in  
XX CC treating tumours, especially in tandem with interferon. The  
XX CC encoding sequence may be used to create plasmid pTrpXAPNF, allowing  
XX CC transformation of an E.coli host for the expression of TNF.  
XX SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;  
XX Query Match 100.0%; Score 43; DB 7; Length 1323;  
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTGA 43  
DB 754 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTGA 796  
RESULT 12  
AAF21085  
ID AAF21085 standard; DNA; 1324 BP.  
XX AAF21085;  
XX 14-MAR-2001 (first entry)  
XX Human low adenosine antisense oligonucleotide related sequence #2652.  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX Homo sapiens.  
XX WO200062736-A2.  
XX 26-OCT-2000.  
XX 24-MAR-2000; 2000WO-US08020.  
XX 06-APR-1999; 99US-0127958.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX (NYCE/) NYCE J W.  
XX Nyce JW;  
XX WPI; 2000-679539/66.  
XX Low adenosine (A) content antisense oligonucleotides which do not  
XX trigger adenosine receptors during metabolism, useful e.g. for treating  
XX cancers and respiratory obstructions -  
XX Disclosure; Page 887; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (I) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
XX The antisense oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasoactive peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisense oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction  
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
XX and/or surfactant hypoproduction which are associated with a disease or  
XX condition selected from pulmonary vasoconstriction, inflammation,  
XX allergies, asthma, impeded respiration, respiratory distress syndrome  
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,  
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
XX fragments and antisense oligonucleotides used in the exemplification of  
XX the present invention.  
XX SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;  
XX Query Match 100.0%; Score 43; DB 21; Length 1324;  
XX Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
XX Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTGA 43  
DB 755 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTGA 797  
RESULT 13  
AAA34963  
ID AAA34963 standard; DNA; 1324 BP.  
XX AAA34963;  
XX 28-JUL-2000 (first entry)  
XX Human adenosine receptor related polynucleotide SEQ ID NO:2652.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX Homo sapiens.  
XX WO200009525-A2.  
XX 24-FEB-2000.  
XX 03-AUG-1999; 99WO-US17712.  
XX 03-AUG-1998; 98US-0095212.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX

PI Nyce JW;  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers  
PS Disclosure; Page 814-815; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of  
CC the ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing the  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
XX given in the sequence listing.  
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 21; Length 1324;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797  
  
RESULT 14  
AAN80219  
ID AAN80219 standard; DNA; 1560 BP.  
XX  
AC AAN80219;  
XX  
DT 28-DEC-1990 (first entry)  
XX  
DE Sequence of pE4 encoding human tumour necrosis factor (TNF).  
XX  
KW Lymphokine; antitumour; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 86..313  
FT mat\_peptide /\*tag= a  
FT /\*tag= b  
XX  
PN WO8806625-A.  
XX  
PD 07-SEP-1988.  
XX  
PF 25-JAN-1988; 88WO-US00183.

XX  
PR 26-FEB-1987; 87US-0019221.  
XX  
PA (CETU ) CETUS CORP.  
XX  
PI Mark DF, Thomson JW, Lin LS, Yamamoto R;  
XX  
DR WPI; 1988-271165/38.  
DR P-PSDB; AAP80728.  
XX  
PT Human tumour necrosis factor muteins -  
PT having comparable biological activity with improved stability  
PT and ease of purification  
XX  
PS Disclosure; Fig 1-1 to 1-2; 51pp; English.  
XX  
CC A human TNF protein which is modified from the sequence shown in  
CC AAP80728, including naturally occurring allelic variants is claimed. Also  
CC claimed are: recombinant DNA sequences encoding the protein (AAN80219)  
CC and control sequences for expression; a vector; a transformed host cell;  
CC a method of producing the protein by culturing the host cell;  
CC pharmaceutical compsn. of the protein and a carrier and a method of  
CC treating tumour burden with the compsn. The muteins are capable of the  
CC range of biological activities exhibited by native TNF but exhibit  
CC improved stability and ease of purification.  
XX  
SQ Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 9; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049  
  
RESULT 15  
AAN60557  
ID AAN60557 standard; DNA; 1585 BP.  
XX  
AC AAN60557;  
XX  
DT 28-JUL-1991 (first entry)  
XX  
DE Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.  
XX  
KW Antitumour; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 86..313  
FT mat\_peptide /\*tag= a  
FT /\*tag= b  
XX  
PN WO8604606-A.  
XX  
PD 14-AUG-1986.  
XX  
PF 03-FEB-1986; 86WO-US00236.  
XX  
PR 07-FEB-1985; 85US-0698939.  
PR 19-OCT-1982; 82US-0435154.  
PR 15-APR-1983; 83US-0486162.  
PR 20-DEC-1983; 83US-0564224.  
PR 15-OCT-1984; 84US-0661026.  
PR 07-FEB-1985; 85US-0695934.  
XX  
PA (CETU ) CETUS CORP.  
XX  
PI Mark DF, Lin LS, Lu SDY, Wang AM;

XX WPI; 1986-225458/34.  
DR P-PSDB; AAP60655.  
XX  
PT New synthetic muteins of human tumour necrosis factor protein -  
PT are obtd. by direct mutagenesis and retain antitumour activity  
XX  
PS Disclosure; Fig 1; 47pp; English.  
XX  
CC The sequence encoding TNF produced by the promyelocytic leukemia  
CC cell line (HL-60, ATCC no. CCL240) has been cloned and expressed in  
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in  
CC the TNF sequence appears to be involved in disulphide linkages. The  
CC patentors claim a novel synthetic mutein of a biologically active  
CC hTNF protein, having at least one cysteine residue free from a  
CC disulphide link and non-essential to the activity and having at  
CC least one of the cysteine residues deleted or replaced by another AA.  
CC Plasmid pAW731 (Ser 69) is claimed.  
XX  
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;  
  
Query Match 100.0%; Score 43; DB 7; Length 1585;  
Best local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

Search completed: February 3, 2004, 04:47:56  
Job time : 120.054 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 04:34:02 ; Search time 2465.58 Seconds  
(without alignments)  
1025.182 Million cell updates/sec

Title: US-09-801-371A-1  
Perfect score: 104  
Sequence: 1 gaattcaactggggcctcc.....ggtctgtgcagaatgctgc 104

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_mam: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	474	13 BX118951	BX118951 BX118951
2	104	100.0	630	14 CB528492	CB528492 UI-H-FT2-
3	104	100.0	645	14 CD370363	CD370363 UI-H-FT1-
4	104	100.0	688	14 CD367676	CD367676 UI-H-FT1-

C 5	104	100.0	696	14 CA307225	CA307225 UI-H-FT1-
C 6	104	100.0	699	14 CD364761	CD364761 UI-H-FT2-
C 7	104	100.0	703	14 CD368142	CD368142 UI-H-FT1-
C 8	104	100.0	713	14 CA308256	CA308256 UI-H-FT1-
C 9	104	100.0	719	14 CB528694	CB528694 UI-H-FT2-
C 10	104	100.0	722	12 BQ007008	BQ007008 UI-H-FT1-
C 11	104	100.0	722	14 CA307062	CA307062 UI-H-FT1-
C 12	104	100.0	722	14 CD364988	CD364988 UI-H-FT2-
C 13	104	100.0	723	14 CA308777	CA308777 UI-H-FT1-
C 14	104	100.0	723	14 CD368116	CD368116 UI-H-FT1-
C 15	104	100.0	724	14 CA309711	CA309711 UI-H-FT1-
C 16	104	100.0	726	14 CA310368	CA310368 UI-H-FT1-
C 17	104	100.0	726	14 CD368929	CD368929 UI-H-FT1-
C 18	104	100.0	742	14 CA309509	CA309509 UI-H-FT1-
C 19	104	100.0	744	14 CD366187	CD366187 UI-H-FT1-
C 20	104	100.0	748	14 CA306559	CA306559 UI-H-FT1-
C 21	104	100.0	1201	9 AL543083	AL543083 AL543083
C 22	103	99.0	248	14 T29839	T29839 EST97164 Hu
C 23	103	99.0	693	14 CD367625	CD367625 UI-H-FT1-
C 24	102.4	98.5	684	14 CA307429	CA307429 UI-H-FT1-
C 25	102.4	98.5	713	14 CA309664	CA309664 UI-H-FT1-
C 26	102.4	98.5	718	14 CD367794	CD367794 UI-H-FT1-
C 27	100.8	96.9	672	14 CD367664	CD367664 UI-H-FT1-
C 28	86	82.7	581	9 AI242177	AI242177 qh81g08.x
C 29	85	81.7	561	10 BG232086	BG232086 naf32e06.
C 30	68.2	65.6	583	14 CA748748	CA748748 UI-H-FT1-
C 31	61.4	59.0	1011	9 AL575811	AL575811 AL575811
C 32	61.2	58.8	564	9 AA699697	AA699697 zi78f12.s
C 33	60.8	58.5	562	9 AA207062	AA207062 zr87b03.s
C 34	48.2	46.3	546	9 AA824594	AA824594 oc83d11.s
C 35	34.8	33.5	136	28 B38591	B38591 HS-1047-B2-
C 36	32.6	31.3	691	9 AL110410	AL110410 DKF2p434K
C 37	32.6	31.3	888	13 BQ232100	BQ232100 AGENCOURT
C 38	32.2	31.0	342	10 BF407522	BF407522 UI-R-BJ2-
C 39	31.8	30.6	876	29 CNS001YJ	AL075400 Drosophi1
C 40	30.4	29.2	430	14 CA563031	CA563031 K0308C04-
C 41	30.4	29.2	446	10 BB840094	BB840094 BB840094
C 42	30.4	29.2	452	9 AI286591	AI286591 uk04d09.Y
C 43	30.4	29.2	480	14 CA568528	CA568528 K0428H07-
C 44	30.4	29.2	497	14 CA564319	CA564319 K0324G08-
C 45	30.4	29.2	504	14 CA563286	CA563286 K0312B07-

ALIGNMENTS

RESULT 1  
BX118951  
LOCUS  
DEFINITION  
BX118951 Soares fetal heart NBHH19W Homo sapiens cDNA clone  
IMAGE:1693595, mRNA sequence.  
ACCESSION  
BX118951  
VERSION  
BX118951.1 GI:27882696  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 474)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
TITLE  
Human Unigeneset - RZPD3  
JOURNAL  
Unpublished  
COMMENT  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGE:1693595  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany



Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.

## FEATURES

source

Location/Qualifiers

1. .474  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE998L124300 ; IMAGE:1693595"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NbHH19W"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

BASE COUNT 112 a 118 c 113 g 131 t

## ORIGIN

Query Match 100.0%; Score 104; DB 13; Length 474;  
Best Local Similarity 100.0%; Pred. No. 5.5e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60

Db 65 GAATTCAAACTGGGGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 124

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

Db 125 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 168

## RESULT 2

CB528492/c

## LOCUS

UI-H-FT2-bjd-e-20-0-UI.s1 NCI CGAP\_FT2 Homo sapiens cDNA clone

UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.

## ACCESSION

CB528492

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens

## REFERENCE

AUTHORS

## TITLE

Tumor Gene Index

## JOURNAL

Unpublished

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/cgap.html  
The following repetitive elements were found in this cDNA  
sequence: 1-29, >AT rich#Low\_complexity (matched complement)  
205-279, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1. .630  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjd-e-20-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FT2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP\_FT2 is a subtracted cDNA library constructed from  
a pool of 81 RNA samples from Alveolar Macrophages  
challenged with different treatments. The library was  
subtracted according to Bonaldo, Lennon and Soares, Genome  
Research, 6:791-806, 1996. The tissue was provided by Dr.  
Gary W. Hunninghake of the University of Iowa.  
TAG LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 180 a 137 c 139 g 174 t

## ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 630;  
Best Local Similarity 100.0%; Pred. No. 6.2e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60

Db 503 GAATTCAAACTGGGGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 444

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

Db 443 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 400

## RESULT 3

CD370363/c

## LOCUS

DEFINITION

UI-H-FT1-bkb-n-03-0-UI.s1 NCI CGAP\_FT1 Homo sapiens cDNA clone

UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.

## ACCESSION

CD370363

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens

## REFERENCE

AUTHORS

## TITLE

Tumor Gene Index

## JOURNAL

Unpublished

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 294-368, &gt;(TAAA)n#Simple\_repeat

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1. .645  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bkb-n-03-0-UI"

/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
BASE COUNT 191 a 145 c 144 g 165 t  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 645;  
Best Local Similarity 100.0%; Pred. No. 6.3e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60  
Db 592 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 533  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104  
Db 532 GAATCTGGAGACCAAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 489

RESULT 4  
LOCUS CD367676 688 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-FT1-bjr-1-14-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.  
ACCESSION CD367676.1 GI:31151766  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 688)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 69-143, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.  
FEATURES  
source  
1..688  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

Location/Qualifiers  
1..688  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

/clone="UI-H-FT1-bjr-1-14-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"  
BASE COUNT 176 a 148 c 181 g 183 t  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 688;  
Best Local Similarity 100.0%; Pred. No. 6.4e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60  
Db 367 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 308  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104  
Db 307 GAATCTGGAGACCAAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 264

RESULT 5  
LOCUS CA307225/c  
DEFINITION UI-H-FT1-bhu-n-04-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.  
ACCESSION CA307225  
VERSION CA307225.1 GI:24470279  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 696)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 296-370, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.  
FEATURES  
source  
1..696  
/organism="Homo sapiens"  
/mol\_type="mRNA"

Location/Qualifiers  
1..696  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bjm-n-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 198 a 155 c 160 g 181 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 696;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 594 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 535

QY 61 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 534 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 491

RESULT 6  
LOCUS CD364761/c 699 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone  
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.

ACCESSION CD364761.1 GI:31148851  
VERSION EST.

KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 699)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA sequence: 296-370, >(TAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source Location/Qualifiers  
1..699  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjm-j-11-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT2 is a substracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 200 a 157 c 160 g 182 t  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 699;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 594 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 535

QY 61 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 534 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 491

RESULT 7  
LOCUS CD368142/c 703 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone  
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.

ACCESSION CD368142  
VERSION EST.  
KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 703)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA sequence: 298-372, >(TAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source Location/Qualifiers  
1..703  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bjv-e-20-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-Ft1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 197 a 158 c 161 g 185 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 703;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 596 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 537  
|||||  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGTTCTGGCCAGAATGCTGC 104  
|||||  
Db 536 GAATCTGGAGACCAAGGAGCCTTTGTTCTGGCCAGAATGCTGC 493  
|||||

RESULT 8  
CA308256/c  
LOCUS  
DEFINITION UI-H-Ft1-bhy-e-14-0-UI-s1 NCI\_CGAP\_Ft1 Homo sapiens cDNA clone  
UI-H-Ft1-bhy-e-14-0-UI 3', mRNA sequence.  
ACCESSION CA308256  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 713)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 296-370, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..713  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-Ft1-bhy-e-14-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"

/clone lib="NCI\_CGAP\_Ft1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-Ft1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 164 c 161 g 184 t 1 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 713;  
Best Local Similarity 100.0%; Pred. No. 6.5e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 594 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 535  
|||||  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGTTCTGGCCAGAATGCTGC 104  
|||||  
Db 534 GAATCTGGAGACCAAGGAGCCTTTGTTCTGGCCAGAATGCTGC 491  
|||||

RESULT 9  
CB528694/c  
LOCUS  
DEFINITION UI-H-FT2-bjd-1-22-0-UI-s1 NCI\_CGAP\_FT2 Homo sapiens cDNA clone  
UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.  
ACCESSION CB528694  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 719)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 294-368, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
Location/Qualifiers  
1..719  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjd-1-22-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"



/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT2"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.  
TAG\_LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 163 c 163 g 188 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 719;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 592 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 533  
QY 61 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 532 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 489

RESULT 10  
BQ007008/c  
LOCUS  
DEFINITION  
IMAGE:5846517 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1. .722  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5846517"  
/tissue\_type="Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_E11"  
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is  
ACACTTGCAC.

TAG\_LIB=UI-H-E11  
TAG\_TISSUE=chondrosarcoma  
TAG\_SEQ=ACACTTGCAC"

BASE COUNT 204 a 162 c 164 g 190 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 12; Length 722;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 595 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536  
QY 61 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 535 GAATCTGGAGACCCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 492

RESULT 11  
CA307062/c  
LOCUS  
DEFINITION  
IMAGE:5846517 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bentos-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 295-369, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Location/Qualifiers  
1. .722  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bhu-o-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome

Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Alveolar Macrophage  
TAG\_SEQ=GGCCATGCCG

BASE COUNT 203 a 165 c 163 g 189 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 722;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 593 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 534

OY 61 GAATCTGGAGACCGAGGCGCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 533 GAATCTGGAGACCGAGGCGCTTTGGTTCTGGCCAGAAATGCTGC 490

RESULT 12  
CD364988/c  
LOCUS CD364988 722 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-FT2-bjn-c-04-0-UI.s1 NCI CGAP\_FT2 Homo sapiens cDNA clone  
UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.

ACCESSION CD364988  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 722)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information/cgap.html  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Source  
Location/Qualifiers  
1..722  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjn-c-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="NCI CGAP FT2"  
/clone\_lib="NCI CGAP FT2"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI CGAP FT2 is a substracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was

subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG LIB=UI-H-FT2  
TAG\_TISSUE=Human Lung Alveolar Macrophage  
TAG\_SEQ=GGCCATGCCG

BASE COUNT 201 a 166 c 163 g 190 t 2 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 722;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 595 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

OY 61 GAATCTGGAGACCGAGGCGCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 535 GAATCTGGAGACCGAGGCGCTTTGGTTCTGGCCAGAAATGCTGC 492

RESULT 13  
CA308777/c  
LOCUS CA308777 723 bp mRNA linear EST 01-NOV-2002  
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP\_FT1 Homo sapiens cDNA clone  
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.

ACCESSION CA308777  
VERSION CA308777.1 GI:24471831  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 723)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Source  
Location/Qualifiers  
1..723  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bhy-b-23-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="NCI CGAP FT1"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.  
Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 164 c 191 t 1 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 723;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 595 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536  
|||||

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 535 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 492  
|||||

RESULT 14  
CD368116/c  
LOCUS  
DEFINITION  
UI-H-FT1-bjv-a-04-0-UI.s1 723 bp mRNA linear EST 29-MAY-2003  
UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 723)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/cgap.html>  
The following repetitive elements were found in this cDNA  
sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

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source  
1. .723  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bjv-a-04-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the

synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 205 a 164 c 164 g 190 t  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 723;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 595 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536  
|||||

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||||  
Db 535 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 492  
|||||

RESULT 15  
CA309711/c  
LOCUS  
DEFINITION  
UI-H-FT1-bic-b-17-0-UI.s1 724 bp mRNA linear EST 01-NOV-2002  
UI-H-FT1-bic-b-17-0-UI 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 724)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA sequence: 297-371, >(TAAA)n#Simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1. .724  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT1-bic-b-17-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP FT1"  
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into

pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG LIB=UI-H-FT1  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_SEQ=GGCCATGCCG"

BASE COUNT 203 a 166 c 164 g 190 t 1 others  
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 724;  
Best Local Similarity 100.0%; Pred. No. 6.6e-21;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGTTGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
595 GAATTCAAACCTGGGGCTCCAGAACTCACTGTTGGGCTTACAGCTTTGATCCCTGACATCTG 536

QY 61 GAATCTGGAGACAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
535 GAATCTGGAGACAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 492

Search completed: February 3, 2004, 06:12:17  
Job time : 2472.58 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: February 3, 2004, 03:36:36 ; Search time 450.769 Seconds  
(without alignments)  
3902.476 Million cell updates/sec

Title: US-09-801-371A-2  
Perfect score: 43  
Sequence: 1 tcaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43	100.0	400	11	G13533	G13533 SHGC-11076
2	43	100.0	787	6	AR300453	AR300453 Sequence
3	43	100.0	787	6	BD070551	BD070551 Self-regu
4	43	100.0	787	6	BD137681	BD137681 Self-regu
5	43	100.0	817	6	AI6444	AI6444 Xho-PstI fr
6	43	100.0	817	6	E02109	E02109 DNA sequenc
7	43	100.0	1047	9	HSA249755	AJ249755 Homo sapi
8	43	100.0	1275	6	I08430	I08430 Sequence 5
9	43	100.0	1323	6	I07953	I07953 Sequence 6
10	43	100.0	1324	6	E00702	E00702 CDNA encodi
11	43	100.0	1324	6	I03610	I03610 Sequence 2
12	43	100.0	1379	12	SYNTNFTRP	M35592 Synthetic h
13	43	100.0	1465	6	I04244	I04244 Sequence 2
14	43	100.0	1560	6	I08863	I08863 Sequence 3
15	43	100.0	1585	6	A37272	A37272 Sequence 12
16	43	100.0	1585	6	I04169	I04169 Sequence 1
17	43	100.0	1585	6	I04198	I04198 Sequence 1
18	43	100.0	1585	6	I08384	I08384 Sequence 5
19	43	100.0	1585	6	I08429	I08429 Sequence 3
20	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor
21	43	100.0	1606	6	I07541	I07541 Sequence 22
22	43	100.0	1643	6	AR146199	AR146199 Sequence
23	43	100.0	1643	9	HSTNFR	X01394 Human mRNA
24	43	100.0	1676	9	BC028148	BC028148 Homo sapi
25	43	100.0	2270	6	AR300459	AR300459 Sequence
26	43	100.0	2270	6	BD137687	BD137687 Self-regu
27	43	100.0	2570	6	AR300460	AR300460 Sequence
28	43	100.0	2570	6	BD137688	BD137688 Self-regu
29	43	100.0	3103	9	HUMTNFX	M26331 Human tumor
30	43	100.0	3634	6	AR100270	AR100270 Sequence
31	43	100.0	3634	6	AR149925	AR149925 Sequence
32	43	100.0	3634	6	BD064008	BD064008 Novel exp
33	43	100.0	3634	9	HSTNFA	X02910 Human gene
34	43	100.0	4830	9	AY066019	AY066019 Homo sapi
35	43	100.0	6974	9	AB088112	AB088112 Homo sapi
36	43	100.0	7112	6	AX100950	AX100950 Sequence
37	43	100.0	7112	6	AX100965	AX100965 Sequence
38	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor
39	43	100.0	7240	9	AY214167	AY214167 Homo sapi
40	43	100.0	16310	9	HSTNFABX	Z15026 Homo sapien
41	43	100.0	40160	9	BX248519	BX248519 Human DNA
42	43	100.0	61358	9	AL929587	AL929587 Human DNA
43	43	100.0	81800	9	HSY14768	Y14768 Homo sapien
44	43	100.0	100000	9	AP000505	AP000505 Homo sapi
45	43	100.0	132330	9	AL662801	AL662801 Human DNA

ALIGNMENTS

RESULT 1  
G13533  
LOCUS SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.  
DEFINITION linear STS 30-MAR-2000  
ACCESSION G13533  
VERSION G13533.1 GI:1129272  
KEYWORDS STS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 400)  
Olivier,M. and Cox,D.R.  
Unpublished, Olivier, M., Cox, D.R. (2000)  
JOURNAL Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox  
Stanford Human Genome Center  
Stanford University School of Medicine  
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA  
Tel: (650) 320-5800  
Fax: (650) 320-5801  
Email: olivier@shgc.stanford.edu  
Primer A: CACTAAGAAATCAAACTGGGGC  
Primer B: GAGGAAGGCCTAAGTCCAC  
STS size: 166  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul  
Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

FEATURES

source

STS

primer\_bind 210..375  
primer\_bind complement(356..375) 89 t  
BASE COUNT 104 a 120 c 87 g 89 t

ORIGIN

Query Match 100.0%; Score 43; DB 11; Length 400;  
Best Local Similarity 100.0%; Pred. No. 6.6e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 43  
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Db 220 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 262  
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RESULT 2

AR300453

LOCUS

DEFINITION Sequence 7 from patent US 6537784.

ACCESSION AR300453

VERSION AR300453.1 GI:31687895

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 787)

AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.

TITLE Self-regulated apoptosis of inflammatory cells by gene therapy

JOURNAL Patent: US 6537784-A 7 25-MAR-2003;

FEATURES Location/Qualifiers

source 1..787

/organism="unknown"

BASE COUNT 190 a 204 c 172 g 221 t

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 787;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 43  
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Db 226 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 268  
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RESULT 3

BD070551

LOCUS

DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.

ACCESSION BD070551

VERSION BD070551.1 GI:22616154

KEYWORDS JP 2001516210-A/13.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 787)

AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.

TITLE Self-regulated apoptosis of inflammatory cells by gene therapy

JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;

COMMENT BOEHRINGER INGELHEIM PHARMACEUTICALS INC

OS Unidentified

PN JP 2001516210-A/13

PD 25-SEP-2001

PF 27-FEB-1998 JP 1998537909

PR 28-FEB-1997 US 60/039266

PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC

A61K31/70,C07H21/04,C12N15/12,C12P19/34

CC Strandedness: Single;

CC Topology: Linear;

CC TNF alpha nontranslated region

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FT source 1..787

FT /organism='Unidentified'.

FEATURES

source

1..787

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

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ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 787;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 43  
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Db 226 TCAAACTGGGCCTCCAGAACTCACTGGGCCTACAGCTTTGA 268  
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RESULT 4

BD137681

LOCUS

DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.

ACCESSION BD137681

VERSION BD137681.1 GI:23232626

KEYWORDS JP 2002504381-A/7.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 787)

AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.

TITLE Self-regulated apoptosis of inflammatory cells by gene therapy

JOURNAL Patent: JP 2002504381-A 7 12-FEB-2002;

COMMENT BOEHRINGER INGELHEIM PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002504381-A/7  
PD 12-FEB-2002  
PF 12-JAN-1999 JP 2000533579  
PR 27-FEB-1998 US 60/076316  
PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC  
C12N15/09, A61K31/7088, A61K48/00, A61P1/04, A61P3/10, A61P17/06, PC  
A61P25/00,  
PC A61P29/00, A61P43/00, C12N9/64, C12Q1/68//C12N5/10, C12N15/00, PC  
C12N5/00  
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FH Key Location/Qualifiers  
FT source 1..787  
FT Location/Qualifiers  
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/mol\_type="genomic DNA"  
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BASE COUNT 190 a 204 c 172 g 221 t  
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Query Match 100.0%; Score 43; DB 6; Length 787;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
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Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268  
|||||  
RESULT 5  
A16444  
LOCUS  
DEFINITION Xho-PstI fragment from THP-I cells.  
ACCESSION A16444  
VERSION A16444.1 GI:641014  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Soma, G.I., Mizuno, D., Tsuji, Y. and Kobayashi, N.  
TITLE Anti-aids preparation  
JOURNAL Patent: EP 0450240-A 9 09-OCT-1991;  
Soma, Gen-Ichiro; Mizuno, Den'ichi  
FEATURES  
source  
Location/Qualifiers  
1..817  
/organism="Homo sapiens"  
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BASE COUNT 183 a 268 c 206 g 160 t  
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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
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Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758  
|||||  
RESULT 6  
E02109  
LOCUS  
DEFINITION DNA sequence coding for anti-tumor polypeptide.  
ACCESSION E02109  
VERSION E02109.1 GI:2170351  
KEYWORDS JP 1989256390-A/1.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
1 (bases 1 to 817)  
Soma, G., Mizuno, D. and Tsuji, Y.  
PI NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL  
POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT  
FROM SAID POLYPEPTIDE  
Patent: JP 1989256390-A 1 12-OCT-1989;  
SOMA GENICHIRO, MIZUNO DENICHI  
PN JP 1989256390-A/1  
PD 12-OCT-1989  
PF 03-APR-1988 JP 1988081683  
PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIKI PC  
C12N15/00, A61K37/24, C07K13/00, C12P21/02, (C12P21/02, C12R1:19); CC  
strandedness: Double;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
CC \*source: library=THP-1 cell;  
FH Key Location/Qualifiers  
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/db\_xref="taxon:3847"  
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Best Local Similarity 100.0%; Pred. No. 6.2e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43  
|||||  
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758  
|||||  
RESULT 7  
HSA249755  
LOCUS  
DEFINITION Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3'  
UTR, country United Arab Emirates.  
ACCESSION AJ249755  
VERSION AJ249755.1 GI:6002308  
KEYWORDS TNF-alpha gene; tumor necrosis factor-alpha.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Farhan, A.J., Pravica, V. and Hutchinson, I.V.  
TITLE Identification of new rare variant of human TNF-alpha 3' UTR  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1047)  
AUTHORS Farhan, A.J.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research  
Division, Manchester University, Medical School, Stopford Building,  
Oxford Road, Manchester, M13 9PT, UNITED KINGDOM  
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source  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/country="United Arab Emirates"  
/note="new rare variant"  
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/gene="TNF-alpha"  
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3' UTR

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DEFINITION	CDNA encoding human tumor necrosis factor.			
ACCESSION	E00702			
VERSION	E00702.1	GI:2168979		
KEYWORDS	JP 1986040221-A/1.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 1324)			
TITLE	TUMOR NECROTIC FACTOR			
JOURNAL	Patent: JP 1986040221-A 1 26-FEB-1986;			
COMMENT	GENENTECH INC			
OS	homosapiens			
PN	JP 1986040221-A/1			
PD	26-FEB-1986			
PF	05-JUL-1985	JP 1985149075		
PR	05-JUL-1984	US 84 627959, 05-JUL-1984	US 84 628059, PR	
	05-JUL-1984	US 84 628060, 03-DEC-1984	US 84 677156, PR	
	03-DEC-1984	US 84 677257, 03-DEC-1984	US 84 677454 PI	BARAA
	BUSHIYAN AGAARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII,			
	PI GUREN EBAN NEDOUIN			
PC	A61K35/12, A61K35/02, A61K35/14, A61K35/74, A61K37/04, C07H21/02,			
PC	C07H21/04,			
PC	C12N15/00;			
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CC	topology: Linear;			
CC	hypothetical: No;			
CC	anti-sense: No;			
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DEFINITION	Sequence 2 from Patent US 4650674.			
ACCESSION	I03610			
VERSION	I03610.1	GI:268632		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			



REFERENCE 1 (bases 1 to 1324)  
AUTHORS Aggarwal,B.B. and Lee,S.He.  
TITLE Synergistic cytotoxic composition  
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;  
Genentech, Inc.; SO. San Francisco, CA  
FEATURES Location/Qualifiers  
source 1..1324  
BASE COUNT 298 a 387 c 308 g 331 t  
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Best Local Similarity 100.0%; Pred. No. 6e-07;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS SYNTNFTRP 1379 bp mRNA linear SYN 27-APR-1993  
DEFINITION Synthetic human tumor necrosis factor mRNA, complete cds.  
ACCESSION M35592  
VERSION M35592.1 GI:209485  
KEYWORDS tumor necrosis factor.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 1379)  
AUTHORS Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Morishita,H.,  
Tohyama,J., Andoh,S. and Kurimoto,M.  
TITLE The expression of human tumor necrosis factor in E. coli  
JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)  
MEDLINE 87174864  
PUBMED 3031624  
COMMENT Original source text: Altered human leukemic B-cell line Ball-1,  
CDNA to mRNA, clone pM324-346.  
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mat\_peptide 400..876  
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RESULT 13  
I04244

LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 2 from Patent US 4677197.  
ACCESSION I04244  
VERSION I04244.1 GI:268725  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1465)  
AUTHORS Lin,L.S. and Yamamoto,R.  
TITLE Purification method for tumor necrosis factor  
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;  
Cetus Corporation; Emeryville, CA  
FEATURES Location/Qualifiers  
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Db 887 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 929  
RESULT 14  
I08863  
LOCUS I08863 1560 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 3 from Patent WO 8806625.  
ACCESSION I08863  
VERSION I08863.1 GI:588416  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1560)  
AUTHORS Mark,D.F., Lin,L.S., Thomson,J.W. and Yamamoto,R.  
TITLE ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR  
JOURNAL Patent: WO 8806625-A 3 07-SEP-1988;  
FEATURES Location/Qualifiers  
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BASE COUNT 340 a 473 c 381 g 366 t  
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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 15  
A37272  
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 12 from Patent WO9404196.  
ACCESSION A37272  
VERSION A37272.1 GI:2294369  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Vile,R.G. and Hart,I.R.  
TITLE TUMOUR THERAPY  
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;  
IMP CANCER RES TECH (GB)  
FEATURES Location/Qualifiers

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Job time : 450.769 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 03:36:36 ; Search time 1090.23 Seconds  
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3902.476 Million cell updates/sec

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Perfect score: 104  
Sequence: 1 gaattcaaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: gb\_pl:  
9: gb\_pr:  
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11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
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17: em\_hum:  
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19: em\_mu:  
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21: em\_or:  
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26: em\_ro:  
27: em\_sts:  
28: em\_un:  
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30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
34: em\_htg\_pln:  
35: em\_htg\_rod:  
36: em\_htg\_mam:  
37: em\_htg\_vrt:  
38: em\_sy:  
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40: em\_htgo\_mus:  
41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	104	100.0	787	6	AR300453	AR300453 Sequence
3	104	100.0	787	6	BD070551	BD070551 Self-regu
4	104	100.0	787	6	BD137681	BD137681 Self-regu
5	104	100.0	1275	6	I08430	I08430 Sequence 5
6	104	100.0	1323	6	I07953	I07953 Sequence 6
7	104	100.0	1324	6	E00702	E00702 CDNA encodi
8	104	100.0	1324	6	I03610	I03610 Sequence 2
9	104	100.0	1465	6	I04244	I04244 Sequence 2
10	104	100.0	1585	6	A37272	A37272 Sequence 12
11	104	100.0	1585	6	I04169	I04169 Sequence 1
12	104	100.0	1585	6	I04198	I04198 Sequence 1
13	104	100.0	1585	6	I08384	I08384 Sequence 5
14	104	100.0	1585	6	I08429	I08429 Sequence 3
15	104	100.0	1585	9	HUMTNFAA	M10988 Human tumor
16	104	100.0	1606	6	I07541	I07541 Sequence 22
17	104	100.0	1643	6	ARI46199	ARI46199 Sequence
18	104	100.0	1643	9	HSTNFR	X01394 Human mRNA
19	104	100.0	1676	9	BC028148	BC028148 Homo sapi
20	104	100.0	2270	6	AR300459	AR300459 Sequence
21	104	100.0	2270	6	BD137687	BD137687 Self-regu
22	104	100.0	2570	6	AR300460	AR300460 Sequence
23	104	100.0	2570	6	BD137688	BD137688 Self-regu
24	104	100.0	3103	9	HUMTNFX	M26331 Human tumor
25	104	100.0	3634	6	ARI00270	ARI00270 Sequence
26	104	100.0	3634	6	ARI49925	ARI49925 Sequence
27	104	100.0	3634	6	BD064008	BD064008 Novel exp
28	104	100.0	3634	9	HSTNFA	X02910 Human gene
29	104	100.0	4830	9	AY066019	AY066019 Homo sapi
30	104	100.0	6974	9	AB088112	AB088112 Homo sapi
31	104	100.0	7112	6	AX100950	AX100950 Sequence
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36	104	100.0	40160	9	EX248519	EX248519 Human DNA
37	104	100.0	61358	9	AL929587	AL929587 Human DNA
38	104	100.0	81800	9	HSY14768	Y14768 Homo sapien
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41	104	100.0	135784	9	AL662847	AL662847 Human DNA
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43	104	100.0	212055	2	AP000899	AP000899 Homo sapi
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45	102.4	98.5	817	6	E02109	E02109 DNA sequenc

ALIGNMENTS

RESULT 1  
GI3533  
LOCUS SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.  
DEFINITION  
ACCESSION GI3533  
VERSION GI3533.1 GI:1129272  
KEYWORDS STS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 400)  
AUTHORS Olivier, M. and Cox, D.R.  
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)  
JOURNAL Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox  
Stanford Human Genome Center  
Stanford University School of Medicine  
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA  
Tel: (650) 320-5800  
Fax: (650) 320-5801  
Email: olivier@shgc.stanford.edu  
Primer A: CACTAAGAAATCAAACTGGGGC  
Primer B: GAGGAAGGCCTAAGTCCAC  
STS size: 166  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul  
Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3  
Prepared with primer pairs derived from M10988 -- Unigene.

FEATURES

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QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
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216 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 275  
QY 61 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 104  
Db |||||  
276 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 319  
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LOCUS AR300453 787 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 7 from patent US 6537784.  
ACCESSION AR300453  
VERSION AR300453.1 GI:31687895  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
1 (bases 1 to 787)  
Tatake,R.J., Marlin,S.D. and Barton,R.W.  
Self-regulated apoptosis of inflammatory cells by gene therapy  
Patent: US 6537784-A 7 25-MAR-2003;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

FEATURES

source  
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QY 61 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 104  
Db |||||  
282 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 325  
RESULT 3  
LOCUS BD070551 787 bp DNA linear PAT 27-AUG-2002  
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.  
ACCESSION BD070551  
VERSION BD070551.1 GI:22616154  
KEYWORDS JP 2001516210-A/13.  
SOURCE unidentified  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 787)  
AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.  
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy  
JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;  
BOEHRINGER INGELHEIM PHARMACEUTICALS INC  
COMMENT OS Unidentified  
PN JP 2001516210-A/13  
PD 25-SEP-2001  
PF 27-FEB-1998 JP 1998537909  
PR 28-FEB-1997 US 60/039266  
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC  
A61K31/70,C07H21/04,C12N15/12,C12P19/34  
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CC Topology: Linear;  
CC TNF alpha nontranslated region  
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QY 61 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 104  
Db |||||  
282 GAATCTGGAGACCGAGGAGCCCTTTGGTTCTGTGGCCAGAAATGCTGC 325  
RESULT 4  
LOCUS BD137681 787 bp DNA linear PAT 18-SEP-2002  
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.  
ACCESSION BD137681



VERSION BD137681.1 GI:23232626  
KEYWORDS JP 2002504381-A/7.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 787)  
AUTHORS Tatake,R.J., Marlin,S.D. and Barton,R.W.  
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy  
JOURNAL Patent: JP 2002504381-A 7 12-FEB-2002;  
BOEHRINGER INGELHEIM PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002504381-A/7  
PD 12-FEB-2002  
PF 12-JAN-1999 JP 2000533579  
PR 27-FEB-1998 US 60/076316  
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC  
C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC  
A61P25/00,  
PC A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N5/10,C12N15/00, PC  
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Db 282 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 325  
RESULT 5  
I08430  
LOCUS 108430  
DEFINITION Sequence 5 from Patent WO 8604606.  
ACCESSION I08430  
VERSION I08430.1 GI:588860  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1275)  
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.  
TITLE CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR  
JOURNAL NECROSIS FACTOR PROTEINS  
PATENT: WO 8604606-A 5 14-AUG-1986;  
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source Location/Qualifiers  
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Query Match 100.0%; Score 104; DB 6; Length 1275;  
Best Local Similarity 100.0%; Pred. No. 9.9e-25;  
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Db 693 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 752  
QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 753 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 796  
RESULT 6  
I07953  
LOCUS 107953  
DEFINITION Sequence 6 from Patent EP 0168214.  
ACCESSION I07953  
VERSION I07953.1 GI:589335  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1323)  
AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.  
TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA  
JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;  
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source Location/Qualifiers  
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BASE COUNT 298 a 387 c 308 g 330 t  
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Best Local Similarity 100.0%; Pred. No. 9.9e-25;  
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Db 750 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 809  
QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 810 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 853  
RESULT 7  
E00702  
LOCUS 1324 bp RNA linear PAT 29-SEP-1997  
DEFINITION CDNA encoding human tumor necrosis factor.  
ACCESSION E00702  
VERSION E00702.1 GI:2168979  
KEYWORDS JP 1986040221-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1324)  
AUTHORS Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.  
TITLE TUMOR NECROTIC FACTOR  
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;  
COMMENT GENENTECH INC  
OS homosapiens  
PN JP 1986040221-A/1  
PD 26-FEB-1986  
PF 05-JUL-1985 JP 1985149075  
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR  
05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR  
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA  
BUSHIYAN AGAARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII,  
PI GUREN EBAN NEDOUIN  
PC A61K35/12,A61K35/02,A61K35/14,A61K37/04,C07H21/02,  
PC C07H21/04,  
PC C12N15/00;  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;

CC \*source: cell\_type=promyelocytes;  
CC \*source: cell\_line=HL-60;  
CC \*source: clone=lambda42-4, lambda16-4;  
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FT mat\_peptide 62..532  
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FT <1..535 /product='tumor necrosis factor' FT 3'UTR  
FT 536..>1324.  
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QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 811 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854  
RESULT 8  
I03610  
LOCUS 103610 1324 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 2 from Patent US 4650674.  
ACCESSION I03610  
VERSION I03610.1 GI:268632  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1324)  
AUTHORS Aggarwal,B.B. and Lee,S.He.  
TITLE Synergistic cytotoxic composition  
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;  
Genentech, Inc.; So. San Francisco, CA  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 298 a 387 c 308 g 331 t  
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Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 9  
I04244  
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 2 from Patent US 4677197.  
ACCESSION I04244  
VERSION I04244.1 GI:268725  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1465)  
AUTHORS Lin,L.S. and Yamamoto,R.  
TITLE Purification method for tumor necrosis factor  
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;  
Cetus Corporation; Emeryville, CA  
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source Location/Qualifiers  
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QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 943 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 986  
RESULT 10  
A37272  
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 12 from Patent WO9404196.  
ACCESSION A37272  
VERSION A37272.1 GI:2294369  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Vile,R.G. and Hart,I.R.  
TITLE TUMOUR THERAPY  
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;  
IMP CANCER RES TECH (GB)  
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source Location/Qualifiers  
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Db 1063 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106  
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I04169  
LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 1 from Patent US 4677063.  
ACCESSION I04169  
VERSION I04169.1 GI:268716  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 1585)  
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdell,J.  
TITLE Human tumor necrosis factor  
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;  
Cetus Corporation; Emeryville, CA  
FEATURES  
source  
BASE COUNT 352 a 473 c 389 g 371 t  
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Query Match 100.0%; Score 104; DB 6; Length 1585;  
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RESULT 12  
LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 1 from Patent US 4677064.  
ACCESSION I04198  
VERSION I04198.1 GI:268719  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdell,J.N. and Lin,L.S.  
TITLE Human tumor necrosis factor  
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;  
Cetus Corporation; Emeryville, CA  
FEATURES  
source  
BASE COUNT 352 a 473 c 389 g 371 t  
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Query Match 100.0%; Score 104; DB 6; Length 1585;  
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RESULT 13  
LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 5 from Patent WO 8602381.  
ACCESSION I08384  
VERSION I08384.1 GI:588904  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van Arsdell,J.N.

TITLE HUMAN TUMOR NECROSIS FACTOR  
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;  
FEATURES  
source  
BASE COUNT 352 a 473 c 389 g 371 t  
ORIGIN  
Query Match 100.0%; Score 104; DB 6; Length 1585;  
Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 14  
LOCUS I08429 1585 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 3 from Patent WO 8604606.  
ACCESSION I08429  
VERSION I08429.1 GI:588859  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.  
TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS  
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;  
FEATURES  
source  
BASE COUNT 352 a 473 c 389 g 371 t  
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RESULT 15  
LOCUS HUMTNFAA 1585 bp mRNA linear PRI 14-JAN-1995  
DEFINITION Human tumor necrosis factor (TNF) mRNA.  
ACCESSION M10988  
VERSION M10988.1 GI:339737  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1585)  
AUTHORS Wang,A.M., Creasey,A.A., Ladner,M.B., Lin,L.S., Strickler,J., Van Arsdell,J.N., Yamamoto,R. and Mark,D.F.  
TITLE Molecular cloning of the complementary DNA for human tumor necrosis factor  
JOURNAL Science 228 (4696), 149-154 (1985)  
MEDLINE 85142190

PUBMED 3856324  
COMMENT Original source text: Human cDNA to mRNA, clone pE4.  
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BASE COUNT 352 a 473 c 389 g 371 t  
ORIGIN Chromosome 6p21.3.

Query Match 100.0%; Score 104; DB 9; Length 1585;  
Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 03:10:21; Search time 287.946 Seconds  
(without alignments)  
974.981 Million cell updates/sec

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Perfect score: 104  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	104	21	AZ99816
2	104	100.0	787	20	AZ20979
3	104	100.0	1275	7	AAN60558
4	104	100.0	1323	7	AAN60363
5	104	100.0	1324	21	AAF21085
6	104	100.0	1324	21	AAA34963
7	104	100.0	1560	9	AAN80219
8	104	100.0	1585	7	AAN60557
					Cis-acting nucleot
					Human TNFalpha 3'U
					Sequence encoding
					Sequence encoding
					Human low adenosin
					Human adenosine re
					Sequence of pE4 en
					Sequence encoding

9	104	100.0	1606	7	AAN60446	Sequence encoding
10	104	100.0	1606	17	AAT15424	Human tumour necro
11	104	100.0	1643	17	AAT31021	Human tumour necro
12	104	100.0	1643	24	ABK13195	Human tumour necro
13	104	100.0	1643	25	AAD49644	Human tumour necro
14	104	100.0	1643	25	AAL53712	Tumour necrosis fa
15	104	100.0	2270	20	AZ20983	Chimeric nucleic a
16	104	100.0	2570	20	AZ20984	Chimeric nucleic a
17	104	100.0	3634	19	AAV39005	TNF-alpha gene use
18	104	100.0	3634	20	AAV39005	Tumour necrosis fa
19	104	100.0	3634	21	AAV39005	Human TNF-alpha ge
20	104	100.0	3634	21	AAV39005	Human tumour necro
21	104	100.0	6911	24	AAD45858	Human tumour necro
22	104	100.0	6911	24	AAD45858	Lymphotoxin and tu
23	104	100.0	7112	22	AAF6085	Human tumour necro
24	104	100.0	7112	22	AAF6085	Human tumour necro
25	104	100.0	7112	25	AAV57450	Human tumour necro
26	104	100.0	16310	21	AAF21086	Human low adenosin
27	104	100.0	16310	21	AAF21086	Human adenosine re
28	104	100.0	17634	21	AAF21087	Human low adenosin
29	104	100.0	17634	21	AAF21087	Human low adenosin
30	104	100.0	17634	21	AAA34965	Human adenosine re
31	104	100.0	17634	21	AAA34965	Human adenosine re
32	104	100.0	81800	24	ABK84756	Human cDNA differe
33	102.4	98.5	817	11	AAQ04340	THP-1. Homo sapie
34	102.4	98.5	818	10	AAN91035	XhoI - PstI sectio
35	102.4	98.5	1200	8	AAN70072	Human anti-tumor p
36	102.4	98.5	1200	10	AAN90969	Part of gene for a
37	102.4	98.5	1585	7	AAN60527	Sequence encoding
38	102.4	98.5	1585	15	AAQ58037	Tumour necrosis fac
39	102.4	98.5	1643	8	AAN711307	Sequence encoding
40	91.8	88.3	815	8	AAN70075	Human anti-tumor p
41	50	48.1	50	21	AZ99815	Sequence of the st
42	43	41.3	43	21	AZ99817	Cis-acting nucleot
43	33	31.7	51	21	AZ99916	Sequence of the st
44	31.4	30.2	10240	19	AAV39007	Porcine TNF-alpha
45	30.2	29.0	2980	22	AAK86235	Human immune/haema

ALIGNMENTS

RESULT 1

AZ99816  
ID AZ99816 standard; RNA; 104 BP.

XX AZ99816;

AC AZ99816;

XX 12-JUL-2000 (first entry)

XX Cis-acting nucleotide sequence derived from human TNF-alpha.

DE Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;

XX RNA-activated protein kinase; eukaryotic initiation factor 2; eif2alpha;

XX tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

OS Homo sapiens.

XX WO200014255-A1.

PD 16-MAR-2000.

PF 06-SEP-1999; 99WO-IL00483.

XX 07-SEP-1998; 98IL-0126112.

PR 26-OCT-1998; 98IL-0126757.

XX (YISS ) YISSUM RES & DEV CO.

PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX WPI; 2000-257000/22.

Regulation of gene expression by mRNA splicing is carried out using a cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2 -

Claim 4; Page 15; 75pp; English.

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the invention.

RESULT 2	
AAZ20979	
ID	AAZ20979 standard; DNA; 787 BP.
XX	
XX	AAZ20979;
XX	
DT	30-NOV-1999 (first entry)
XX	
DE	Human TNFalpha 3'UTR.
XX	
KW	TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW	chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW	psoriasis; graft versus host disease; lupus erythematosus;
KW	diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX	
OS	Homo sapiens.
XX	
FN	WO9943840-A1.
XX	
PD	02-SEP-1999.
XX	
PF	12-JAN-1999; 99WO-US00637.
XX	
PR	27-FEB-1998; 98US-0076316.
XX	
PA	(BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX	
PI	Tatake RJ, Marlin SD, Barton RW;
XX	
DR	WPI; 1999-527630/44.
XX	
PT	A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PT	promoter and an apoptosis-inducing Granzyme B polynucleotide -
XX	

Example 1; Page 60-61; 71pp; English.

This sequence represents a human TNFalpha (tumour necrosis factor alpha) 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were constructed comprising at least one TNFalpha promoter enhancer region (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha 3'UTR sequence. TNFalpha is one of a number of cytokines produced by inflammatory cells. Upregulation and/or dysregulation of cytokines in inflamed tissue may be directly or indirectly responsible for exacerbation of chronic inflammatory diseases. Introduction of the chimeric nucleotide to activated inflammatory cells causes them to undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide may be useful for treating inflammatory disorders such as multiple sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus host disease, lupus erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and cheaper long-term relief, in comparison with existing conventional pharmaceutical and invasive surgery methods.

Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

RESULT 3
AAN60558
ID AAN60558 standard; DNA; 1275 BP.
XX AC
XX AAN60558;
XX AC
DT 28-JUL-1991 (first entry)
DE Sequence encoding mature human tumour necrosis factor (htnf) mutein
DE Ser 69 in pAW731.
XX KW Antitumour; anticancer; ss.
OS Homo sapiens.
XX OS
FH Key
FT CDS Location/Qualifiers
FT 1..474
FT /*tag= a
XX XX
PN W08604606-A.
XX XX
PD 14-AUG-1986.
XX XX
Pf 03-FEB-1986; 86WO-US00236.
XX XX
PR 07-FEB-1985; 85US-0698939.
PR 19-OCT-1982; 82US-0435154.
PR 15-APR-1983; 83US-0486162.
PR 20-DEC-1983; 83US-0564224.
PR 15-OCT-1984; 84US-0661026.
PR 07-FEB-1985; 85US-0695934.
XX XX
PA (CETU ) CETUS CORP.
XX XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX XX

DR WPI: 1986-225458/34.  
XX P-PSDB; AAP60656.  
PT New synthetic muteins of human tumour necrosis factor protein -  
PT are obtd. by direct mutagenesis and retain antitumour activity  
XX  
XX Disclosure; Fig 3a; 47pp; English.  
XX  
CC The sequence encoding TNF produced by the promyelocytic leukemia  
CC cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in  
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in  
CC the TNF sequence appears to be involved in disulphide linkages. The  
CC patentors claim a novel synthetic mutein of a biologically active  
CC hTNF protein, having at least one cysteine residue free from a  
CC disulphide link and non-essential to the activity and having at  
CC least one of the cysteine residues deleted or replaced by another AA.  
CC Plasmid pAN731 (Ser 69) is claimed.  
XX  
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;  
Query Match 100.0%; Score 104; DB 7; Length 1275;  
Best Local Similarity 100.0%; Pred. No. 2.7e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60  
Db 693 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 752  
QY 61 GAATCTGGAGACAGGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104  
Db 753 GAATCTGGAGACAGGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 796  
RESULT 4  
AAN60363  
ID AAN60363 standard; DNA; 1323 BP.  
XX  
AC AAN60363;  
XX  
DT 19-JUN-1991 (first entry)  
XX  
DE Sequence encoding human tumour necrosis factor.  
XX  
KW hTNF; tumour; cancer; interferon; ds.  
XX  
OS Homo sapiens.  
XX  
FH Location/Qualifiers  
FT 1..534  
FT /\*tag= a  
FT sig\_peptide 1..60  
FT /\*tag= b  
FT mat\_peptide /label= Secretory leader peptide  
FT 61..534  
FT /\*tag= c  
XX  
PN EP168214-A.  
XX  
PD 15-JAN-1986.  
XX  
PF 03-JUL-1985; 85EP-0304758.  
XX  
PR 03-DEC-1984; 84US-0677454.  
PR 05-JUL-1984; 84US-0627959.  
PR 05-JUL-1984; 84US-0628059.  
PR 05-JUL-1984; 84US-0628060.  
PR 03-DEC-1984; 84US-0677156.  
PR 03-DEC-1984; 84US-0677257.  
PR 25-JUL-1984; 84US-0627969.  
PR 03-DEC-1984; 84US-0677267.  
XX  
PA (GETH ) GENENTECH INC.  
XX

PI Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;  
XX  
DR WPI: 1986-015483/03.  
XX P-PSDB; AAP60417.  
PT Pure tumour necrosis factor and mutant forms - new DNA coding  
PT sequences and transformed cells.  
XX  
XX Claim 20; Fig 10; 90pp; English.  
XX  
CC Sequence encodes the pure human tumour necrosis factor, mutants of  
CC which are covered by the claims. TNF and mutants are useful in  
CC treating tumours, especially in tandem with interferon. The  
CC encoding sequence may be used to create plasmid pTrpXAPTNF, allowing  
CC transformation of an E.coli host for the expression of TNF.  
XX  
SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;  
Query Match 100.0%; Score 104; DB 7; Length 1323;  
Best Local Similarity 100.0%; Pred. No. 2.7e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60  
Db 750 GAATTCAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 809  
QY 61 GAATCTGGAGACAGGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104  
Db 810 GAATCTGGAGACAGGAGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 853  
RESULT 5  
AAF21085  
ID AAF21085 standard; DNA; 1324 BP.  
XX  
AC AAF21085;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2652.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI: 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX

PS Disclosure; Page 887; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

XX SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Query Match 100.0%; Score 104; DB 21; Length 1324;  
Best Local Similarity 100.0%; Pred. No. 2.7e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
751 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
811 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854

RESULT 6  
AAA34963  
ID AAA34963 standard; DNA; 1324 BP.  
XX  
AC AAA34963;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX Nyce JW;  
XX WPI; 2000-205971/18.  
XX New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, or bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -  
XX Disclosure; Page 814-815; 1343pp; English.  
XX The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing the bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

XX SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Query Match 100.0%; Score 104; DB 21; Length 1324;  
Best Local Similarity 100.0%; Pred. No. 2.7e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
751 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
811 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854

RESULT 7  
AAN80219  
ID AAN80219 standard; DNA; 1560 BP.  
XX  
AC AAN80219;  
XX  
DT 28-DEC-1990 (first entry)  
XX  
DE Sequence of pE4 encoding human tumour necrosis factor (TNF).  
XX  
KW Lymphokine; antitumour; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 86..313



FT mat\_peptide /\*tag= a  
FT 314..787  
FT /\*tag= b  
XX  
XX WO8806625-A.  
XX  
XX PN  
XX  
XX PD  
XX 07-SEP-1988.  
XX  
XX PF  
XX 25-JAN-1988; 88WO-US00183.  
XX  
XX PR  
XX 26-FEB-1987; 87US-0019221..  
XX  
XX PA  
XX (CETU ) CETUS CORP.  
XX  
XX PI  
XX Mark DF, Thomson JW, Lin LS, Yamamoto R;  
XX  
XX DR  
XX WPI; 1988-271165/38.  
XX  
XX P-PSDB; AAP80728.  
XX  
XX PT  
XX Human tumour necrosis factor muteins -  
XX having comparable biological activity with improved stability  
XX and ease of purification  
XX  
XX PS  
XX Disclosure; Fig 1-1 to 1-2; 5lpp; English.  
XX  
XX CC  
XX A human TNF protein which is modified from the sequence shown in  
XX AAP80728, including naturally occurring allelic variants is claimed. Also  
XX claimed are: recombinant DNA sequences encoding the protein (AAN80219)  
XX and control sequences for expression; a vector; a transformed host cell;  
XX a method of producing the protein by culturing the host cell;  
XX pharmaceutical compen. of the protein and a carrier and a method of  
XX treating tumour burden with the compen. The muteins are capable of the  
XX range of biological activities exhibited by native TNF but exhibit  
XX improved stability and ease of purification.  
XX  
XX SQ  
XX Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;  
XX  
XX Query Match 100.0%; Score 104; DB 9; Length 1560;  
XX Best Local Similarity 100.0%; Pred. No. 2.8e-25;  
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
XX  
XX Db 1003 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062  
XX  
XX QY 61 GAATCTGGAGACACAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104  
XX  
XX Db 1063 GAATCTGGAGACACAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 1106  
XX  
XX  
XX RESULT 8  
XX AAN60557  
XX ID AAN60557 standard; DNA; 1585 BP.  
XX  
XX AC AAN60557;  
XX  
XX XX  
XX 28-JUL-1991 (first entry)  
XX  
XX DE  
XX Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.  
XX  
XX KW  
XX Antitumour; anticancer; ss.  
XX  
XX XX  
XX Homo sapiens.  
XX  
XX FH  
XX Key Location/Qualifiers  
XX CDS 86..313  
XX FT /\*tag= a  
XX FT 314..787  
XX FT mat\_peptide /\*tag= b  
XX  
XX PN  
XX WO8604606-A.  
XX  
XX PD  
XX 14-AUG-1986.

XX 03-FEB-1986; 86WO-US00236.  
XX  
XX PR  
XX 07-FEB-1985; 85US-0698939.  
XX  
XX PR  
XX 19-OCT-1982; 82US-0435154.  
XX  
XX PR  
XX 15-APR-1983; 83US-0486162.  
XX  
XX PR  
XX 20-DEC-1983; 83US-0564224.  
XX  
XX PR  
XX 15-OCT-1984; 84US-0661026.  
XX  
XX PR  
XX 07-FEB-1985; 85US-0695934.  
XX  
XX PA  
XX (CETU ) CETUS CORP.  
XX  
XX PI  
XX Mark DF, Lin LS, Lu SDY, Wang AM;  
XX  
XX DR  
XX WPI; 1986-225458/34.  
XX  
XX P-PSDB; AAP60655.  
XX  
XX PT  
XX New synthetic muteins of human tumour necrosis factor protein -  
XX are obtd. by direct mutagenesis and retain antitumour activity  
XX  
XX PS  
XX Disclosure; Fig 1; 47pp; English.  
XX  
XX CC  
XX The sequence encoding TNF produced by the promyelocytic leukemia  
XX cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in  
XX E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in  
XX the TNF sequence appears to be involved in disulphide linkages. The  
XX patentors claim a novel synthetic mutein of a biologically active  
XX hTNF protein, having at least one cysteine residue free from a  
XX disulphide link and non-essential to the activity and having at  
XX least one of the cysteine residues deleted or replaced by another AA.  
XX Plasmid pAW731 (Ser 69) is claimed.  
XX  
XX SQ  
XX Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;  
XX  
XX Query Match 100.0%; Score 104; DB 7; Length 1585;  
XX Best Local Similarity 100.0%; Pred. No. 2.8e-25;  
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
XX  
XX Db 1003 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062  
XX  
XX QY 61 GAATCTGGAGACACAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104  
XX  
XX Db 1063 GAATCTGGAGACACAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 1106  
XX  
XX  
XX RESULT 9  
XX AAN60446  
XX ID AAN60446 standard; CDNA; 1606 BP.  
XX  
XX AC AAN60446;  
XX  
XX XX  
XX 25-MAR-2003 (updated)  
XX  
XX DT  
XX 07-AUG-1991 (first entry)  
XX  
XX XX  
XX Sequence encoding tumour necrosis factor (TNF).  
XX  
XX DE  
XX Anticancer agent; antitumour; antimalarial; tumour necrosis factor;  
XX KW ss.  
XX  
XX XX  
XX Homo sapiens.  
XX  
XX FH  
XX Key Location/Qualifiers  
XX CDS 158..859  
XX FT /\*tag= a  
XX FT  
XX XX  
XX WO8603751-A.  
XX  
XX PN  
XX 03-JUL-1986.  
XX  
XX PD  
XX 19-DEC-1985; 85WO-EP00721.  
XX  
XX PF  
XX

PR 09-OCT-1985; 85US-0785847.  
PR 21-DEC-1984; 84US-0684595.  
PR 09-OCT-1986; 86WO-US02133.

XX (BIOJ ) BIOGEN NV.  
PA (FIER/) FIER W C.  
PA (ALLE/) ALLET B.  
PA (BIOJ ) BIOGEN INC.

XX Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM;  
PI VanDerHeyden J, Allet B, Washima EH;

XX WPI; 1986-182891/28.  
DR P-PSDB; AAP60531.

XX Mammalian tumour necrosis factors - produced by culturing  
PT pro-karyotic hosts transformed with recombinant DNA

XX Example; Fig 9; 93pp; English.

XX TNF-like polypeptides and compens. are produced by the fermentation  
CC of host cells transformed with at least one DNA sequence which codes  
CC for a mammalian TNF-like polypeptide operatively linked to an  
CC expression control sequence in the transformed host.  
CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

Query Match 100.0%; Score 104; DB 7; Length 1606;  
Best Local Similarity 100.0%; Pred. No. 2.8e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60  
Db 1075 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104

Db 1135 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1178

## RESULT 10

AAT15424  
ID AAT15424 standard; cDNA; 1606 BP.

XX AC AAT15424;

XX DT 25-MAR-2003 (updated)

XX DT 23-APR-1996 (first entry)

XX DE Human tumour necrosis factor cDNA clone p-hTNF-1.

XX KW Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;  
XX KW antitumour; anticancer; antimalarial; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 158..859

FT /\*tag= a

FT sig\_peptide 158..385

FT /\*tag= b

FT mat\_peptide 386..856

FT /\*tag= c

XX US5487984-A.

XX PD 30-JAN-1996.

XX PF 20-DEC-1985; 85US-0811654.

XX PR 20-DEC-1985; 85US-0811654.

XX PR 21-DEC-1984; 84US-0684595.

PR 09-OCT-1985; 85US-0785847.

XX (BIOJ ) BIOGEN INC.

XX Allet B, Kawashima EH;

XX WPI; 1996-105230/11.

DR P-PSDB; AAR88590.

XX Prodn. of tumour necrosis factor - using recombinant DNA encoding  
PT TNF under the control of T4 or lambda pL-T4 expression control  
PT sequences.

XX Example 9; Fig 9; 43pp; English.

XX A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human  
CC tumour necrosis factor (hTNF) precursor (AAR88590). It was obtd.  
CC by screening a human cDNA library with a fragment of mouse TNF  
CC cDNA. The isolated cDNA may be linked to expression control  
CC sequences from phage T4 or phage lambda (see AAT15402-05 and  
CC AAT15425-26) for expression in host cells, esp. Escherichia coli,  
CC and commercial-scale prodn. of recombinant TNF of use as an  
CC antitumour, anticancer and antimalarial agent.  
CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

Query Match 100.0%; Score 104; DB 17; Length 1606;

Best Local Similarity 100.0%; Pred. No. 2.8e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

Db 1075 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104

Db 1135 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1178

## RESULT 11

AAT31021

ID AAT31021 standard; DNA; 1643 BP.

XX AC AAT31021;

XX DT 26-SEP-1996 (first entry)

XX DE Human tumour necrosis factor cDNA clone HSTNFR.

XX KW Gene therapy; hypoxia related enhancer element; HREE; ischaemia;  
XX KW reperfusion; promoter; tumour necrosis factor; TNF; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 153..854

FT /\*tag= a

XX WO9620276-A1.

XX PD 04-JUL-1996.

XX PF 13-NOV-1995; 95WO-IB00996.

XX PR 23-DEC-1994; 94US-0365486.

XX (STRI ) SRI INT.

XX PI Bishopric NH, Green CJ, Laderoute KR, Murphy B;  
XX PI Webster KA;

XX DR WPI; 1996-321849/32.

DR P-PSDB; AAW00454.  
XX  
PT Chimeric gene contg. therapeutic gene linked to HREE - partic. for  
PT expressing SOD etc. in hypoxic tissue to reduce tissue injury caused  
PT by ischaemia or reperfusion  
XX  
PS Example 8; Page 100-101; 118pp; English.  
XX  
CC A PCR-generated DNA fragment (AAT31021) encoding human tumour  
CC necrosis factor (htNF) (AAW00454). htNF induces apoptosis and  
CC is not known to be induced by hypoxic stress. A -90 bp human  
CC metallothionein IIA promoter fragment (see also AAT31003) was  
CC inserted upstream of the htNF gene and the construct was used  
CC to transfect mouse C2C12 myoblasts and A431 cells. Hypoxia-  
CC mediated TNF induction and tumour control were demonstrated  
CC in an animal xenograft model.  
XX  
SQ Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;  
  
Query Match 100.0%; Score 104; DB 17; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129  
|||||  
QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTTGGCCAGAAATGCTGC 104  
|||||  
Db 1130 GAATCTGGAGACCAGGAGCCCTTGGTTCTTGGCCAGAAATGCTGC 1173  
|||||

RESULT 12  
ABK13195  
ID ABK13195 standard; DNA; 1643 BP.  
AC ABK13195;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE Human tumour necrosis factor alpha (TNF alpha) DNA.  
XX  
KW TNF; apoptosis; ds; tumour; death domain receptor ligand;  
KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1;  
KW carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;  
KW neurological malignancy; haematological malignancy; lichen planus;  
KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;  
KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;  
KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;  
KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;  
KW discoid lupus erythematosus; human; gene; tumour necrosis factor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 153..854  
FT /\*tag= a  
FT /product= "TNF alpha protein"  
XX  
PN US6329148-B1.  
XX  
PD 11-DEC-2001.  
XX  
PF 15-FEB-2000; 2000US-0505250.  
XX  
PR 16-FEB-1999; 99US-120313P.  
PR 20-AUG-1999; 99US-149989P.  
XX  
PA (STRD ) UNIV LELAND STANFORD.  
XX  
PI Rosen GD, Kao P;  
XX  
DR WPI; 2002-121125/16.

DR P-PSDB; AAU75065.  
XX  
PT Use of a synergistic combination of death domain receptor ligands and  
PT diterpenoid triepoxides for killing of tumour cells -  
XX  
PS Disclosure; Column 27-30; 20pp; English.  
XX  
CC This invention relates to a novel method for enhanced killing of tumour  
CC cells comprising contacting a tumour cell with a synergistic  
CC combination of a death domain receptor ligand and a diterpenoid  
CC triepoxide. This method has cytostatic activity and works by blocking  
CC TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the  
CC invention may be used for treating tumours, particularly solid tumours,  
CC e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma  
CC also neurological malignancies, haematological malignancies, e.g.  
CC non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant  
CC cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,  
CC lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,  
CC bullous pemphigoid, discoid lupus erythematosus, lichen planus. The  
CC combination may be administered with other active agents, e.g. anti-  
CC metastatic, anti-tumour or anti-angiogenic agents. The potent synergy  
CC between the diterpenoids and the death domain ligands allows increased  
CC killing at equivalent or lower doses, and can sensitize otherwise  
CC resistant cells. This sequence represents the human tumour necrosis  
CC factor alpha (TNF alpha) DNA. TNF alpha is a ligand for death  
CC domain receptors used in the used method of the invention in  
CC combination with diterpenoid triepoxides to kill tumours by  
CC induction of apoptosis.  
XX  
SQ Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;  
  
Query Match 100.0%; Score 104; DB 24; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129  
|||||  
QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTTGGCCAGAAATGCTGC 104  
|||||  
Db 1130 GAATCTGGAGACCAGGAGCCCTTGGTTCTTGGCCAGAAATGCTGC 1173  
|||||  
  
RESULT 13  
AAD49644  
ID AAD49644 standard; DNA; 1643 BP.  
XX  
AC AAD49644;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE Human tumour necrosis factor alpha (TNF-alpha) DNA.  
XX  
KW Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;  
KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;  
KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;  
KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;  
KW haemostatic; antibacterial; nootropic; neuroprotective; cytostatic;  
KW fungicide; human; tumour necrosis factor alpha; TNF-alpha; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
5'UTR 1..152  
FT /\*tag= a  
FT 852..1643  
FT /\*tag= b  
XX  
PN WO200283953-A1.  
XX  
PD 24-OCT-2002.  
XX

PF 11-APR-2002; 2002WO-US11757.

XX 11-APR-2001; 2001US-282965P.

XX (PTCT-) PTC THERAPEUTICS INC.

XX Rando R, Welch E;

XX WPI; 2003-075561/07.

XX Identifying a test compound that binds to a target RNA molecule for  
PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,  
PT diabetes, by contacting a detectably labeled target RNA molecule with a  
PT library of test compounds -

XX Example; Page 53-54; 152pp; English.

XX The invention relates to a method for identifying a test compound that  
CC binds to a target RNA molecule, which comprises contacting a detectably  
CC labelled target RNA molecule with a library of test compounds under  
CC conditions that permit direct binding of the labelled target RNA to a  
CC member of the library of test compounds so that a detectably labeled  
CC target RNA: test compound complex is formed. The method is useful for  
CC screening libraries of compounds for those that are selectively bind to  
CC a pre-selected target RNA. The compounds are useful for inhibiting the  
CC formation of a specific bound RNA: host cell factor complexes in vivo.  
CC They are also useful for treating or preventing diseases associated  
CC with overproduction or decreased protein function, such as amyloidosis,  
CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,  
CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,  
CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative  
CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).  
CC The invention is also used in gene therapy. The present sequence is  
CC human tumour necrosis factor alpha (TNF-alpha) DNA. This sequence  
CC is used to illustrate the method of the invention.

XX Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

Query Match 100.0%; Score 104; DB 25; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
DB 1070 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 14

AAAL53712

ID AAL53712 standard; DNA; 1643 BP.

XX AAL53712;

XX 07-FEB-2003 (first entry)

XX Tumour necrosis factor alpha DNA SEQ ID No 6.

XX Target RNA; target RNA: support-attached test compound; flow cytometry;  
XX mass spectrometry; high-throughput screening; ds.

XX Homo sapiens.

XX WO200283837-A1.

XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US11758.

XX 11-APR-2001; 2001US-282966P.

XX (PTCT-) PTC THERAPEUTICS INC.

XX Almstead NG;

XX WPI; 2003-075534/07.

XX Identifying a test compound that binds to a target RNA molecule by  
PT separating the detectably labeled target RNA: support-attached test  
PT compound complex from uncomplexed target RNA molecules and test  
PT compounds by flow cytometry -

XX Example; Page 44-45; 131pp; English.

XX The invention relates to a novel method for identifying a test compound  
CC that binds to a target RNA molecule comprising separating the detectably  
CC labeled target RNA: support-attached test compound complex from  
CC uncomplexed target RNA molecules and test compounds. The separating  
CC process is carried out by flow cytometry and determining a structure of  
CC the type of test compound of the RNA: support-attached test compound  
CC complex by mass spectrometry. The method is useful for high-throughput  
CC screening of libraries of compounds to identify pharmaceutical leads.  
CC This polynucleotide sequence represents a DNA sequence related to the  
CC detecting method of the invention.

XX Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

Query Match 100.0%; Score 104; DB 25; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
DB 1070 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 15

AAZ20983

ID AAZ20983 standard; DNA; 2270 BP.

XX AAZ20983;

XX 30-NOV-1999 (first entry)

XX Chimeric nucleic acid -706TNFpGB3'UTR.

XX TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;  
XX chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;  
XX psoriasis; graft versus host disease; lupus erythematosus;  
XX diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT promoter 7..733

FT /tag= a

FT /label= TNFalpha promoter

FT /note= "Human TNFalpha native promoter (AAZ20973)"

FT CDS 740..1477

FT /tag= b

FT /product= "Truncated Granzyme B"

FT /note= "Inactivating dipeptide absent"

FT 3'UTR 1490..2264

FT /tag= c

FT /label= TNFalpha\_3'UTR

XX WO9943840-A1.

XX



PD 02-SEP-1999.  
XX  
PF 12-JAN-1999; 99WO-US00637.  
XX  
PR 27-FEB-1998; 98US-0076316.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
XX  
PI Tataka RJ, Marlin SD, Barton RW;  
XX  
DR WPI; 1999-527630/44.  
XX  
PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)  
PT promoter and an apoptosis-inducing Granzyme B polynucleotide -  
XX  
PS Claim 4; Fig 12; 71pp; English.  
XX  
CC This sequence represents chimeric nucleic acid -705TNFpGB3'UTR. This  
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter  
CC enhancer region (AAZ20975-220978), a TNFalpha native promoter (AAZ20973),  
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B  
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)  
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines  
CC produced by inflammatory cells. Upregulation and/or dysregulation  
CC of cytokines in inflamed tissue may be directly or indirectly  
CC responsible for exacerbation of chronic inflammatory diseases.  
CC Introduction of this chimeric nucleotide to activated inflammatory cells  
CC causes them to undergo apoptosis. Pharmaceutical compositions of this  
CC chimeric nucleotide may be useful for treating inflammatory disorders  
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,  
CC psoriasis, graft versus host disease, lupus erythematosus,  
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,  
CC and in particular, rheumatoid arthritis. The use of such chimeric  
CC nucleotides offers simpler and cheaper long-term relief, in comparison  
CC with existing conventional pharmaceutical and invasive surgery methods.  
XX  
SQ Sequence 2270 BP; 556 A; 647 C; 545 G; 522 T; 0 other;

Query Match 100.0%; Score 104; DB 20; Length 2270;  
Best Local Similarity 100.0%; Pred. No. 3.1e-25;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||  
Db 1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1764

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
|||  
Db 1765 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1808

Search completed: February 3, 2004, 04:47:55  
Job time : 290.946 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: February 3, 2004, 04:34:26 ; Search time 80.6531 Seconds  
(without alignments)  
569.152 Million cell updates/sec

Title: US-09-801-371A-1  
Perfect score: 104  
Sequence: 1 gaattcaaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	787	4	US-09-032-297A-13
2	104	100.0	787	4	US-09-329-151C-7
3	104	100.0	1643	3	US-08-880-342-36
4	104	100.0	1643	4	US-09-505-250-4
5	104	100.0	2270	4	US-09-229-151C-13
6	104	100.0	2570	4	US-09-329-151C-14
7	104	100.0	3634	3	US-09-166-186-1
8	104	100.0	3634	3	US-09-313-932-1
9	104	100.0	3634	3	US-09-109-663-34
10	28	26.9	28720	4	US-09-341-587-7
11	27.4	26.3	116592	4	US-09-818-512-3
12	26.4	25.4	3170	4	US-09-169-768-1
13	26.4	25.4	3171	4	US-09-169-768-15
14	26.4	25.4	3181	1	US-08-555-086-1
15	26.4	25.4	3349	4	US-09-169-768-13
16	26.4	25.4	3531	4	US-09-169-768-7
17	26.4	25.4	3541	4	US-09-169-768-9
18	25.8	24.8	3889	4	US-09-484-970B-39
19	25.8	24.8	4031	1	US-08-159-784-1
20	25.6	24.6	642	3	US-09-328-111-82
21	25.6	24.6	1923	4	US-09-620-312D-1004
22	25.6	24.6	2634	3	US-08-911-853-30
23	25.6	24.6	2634	3	US-09-479-409-30
24	25.6	24.6	2634	4	US-09-479-453-30
25	25.6	24.6	17612	3	US-08-911-853-29
26	25.6	24.6	17612	3	US-09-479-409-29
27	25.6	24.6	17612	4	US-09-479-453-29

28	25.4	24.4	220	3	US-09-263-933-22	Sequence 22, Appl
29	25.4	24.4	604	3	US-09-068-880-1	Sequence 1, Appli
30	25.4	24.4	1026	3	US-09-068-880-14	Sequence 14, Appl
31	25.4	24.4	1289	4	US-09-247-155-138	Sequence 138, App
32	25.4	24.4	1467	3	US-09-330-317B-17	Sequence 17, Appl
33	25.4	24.4	1467	4	US-09-808-589A-17	Sequence 17, Appl
34	25.4	24.4	1956	3	US-08-867-352-20	Sequence 20, Appl
35	25.4	24.4	4145	1	US-08-314-917-1	Sequence 1, Appli
36	25.4	24.4	4145	1	US-08-265-046-1	Sequence 1, Appli
37	25.4	24.4	4145	2	US-08-465-522-1	Sequence 1, Appli
38	25.4	24.4	4145	5	PCT-US93-11401-1	Sequence 1, Appli
39	25.4	24.4	4145	5	PCT-US95-07849-1	Sequence 1, Appli
40	25.4	24.4	4951	2	US-08-752-307B-1	Sequence 1, Appli
41	25.4	24.4	4951	4	US-09-707-802-1	Sequence 1, Appli
42	25.4	24.4	4951	4	US-09-991-326-1	Sequence 1, Appli
43	25.4	24.4	7076	4	US-09-837-863-20	Sequence 20, Appl
44	25.4	24.4	7076	4	US-09-837-863-21	Sequence 21, Appl
45	25.4	24.4	7092	4	US-09-837-863-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-09-032-297A-13  
; Sequence 13, Application US/09032297A  
; Patent No. 6525184  
; GENERAL INFORMATION:  
; APPLICANT: Revati J. Tatake, Steven D. Marlin and  
; Randall W. Barton  
; TITLE OF INVENTION: Self-Regulated Apoptosis of  
; Inflammatory Cells by Gene Therapy  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Boehringer Ingelheim Corporation  
; STREET: 900 Ridgebury Road, P.O. Box 368  
; CITY: Ridgefield  
; STATE: Connecticut  
; COUNTRY: United States of America  
; ZIP: 06877-0368  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" 1.44 Mb diskette  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Word Processing  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,297A  
; FILING DATE: 27-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,266  
; FILING DATE: 28-FEB-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robert P. Raymond  
; REGISTRATION NUMBER: 25089  
; REFERENCE/DOCKET NUMBER: 9/121PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203-791-6183  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 787  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: <Unknown>  
; DESCRIPTION: DNA  
; FEATURE:  
; NAME/KEY: TNFa 3', untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-032-297A-13

Query Match 100.0%; Score 104; DB 4; Length 787;  
Best Local Similarity 100.0%; Pred. No. 5.7e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104  
|||||  
Db 282 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325

RESULT 2  
US-09-229-151C-7  
; Sequence 7, Application US/09229151C  
; Patent No. 6537784  
; GENERAL INFORMATION:  
; APPLICANT: Tatake, Revati J.  
; APPLICANT: Marlin, Steven D.  
; APPLICANT: Barton, Randall W.  
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy  
; FILE REFERENCE: 9/137  
; CURRENT APPLICATION NUMBER: US/09/229,151C  
; CURRENT FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: US 60/076,316  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 2.0  
; SEQ ID NO 7  
; LENGTH: 787  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; OTHER INFORMATION: TNF-alpha untranslated region  
US-09-229-151C-7

Query Match 100.0%; Score 104; DB 4; Length 787;  
Best Local Similarity 100.0%; Pred. No. 5.7e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104  
|||||  
Db 282 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325

RESULT 3  
US-08-880-342-36  
; Sequence 36, Application US/08880342  
; Patent No. 6218179  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; APPLICANT: Murphy, Brian  
; APPLICANT: Laderoute, Keith R.  
; APPLICANT: Green, Christopher J.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
; TITLE OF INVENTION: Therapeutic Constructs  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,342  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/IB95/00996  
; FILING DATE: 13-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/365,486  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 8255-0018.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1643 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: TNF cDNA HSTNFR (EMBL Accession  
; INDIVIDUAL ISOLATE: #X01394)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 153..851  
US-08-880-342-36

Query Match 100.0%; Score 104; DB 3; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 7.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
|||||  
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104  
|||||  
Db 1130 GAATCTGGAGACCGAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173

RESULT 4  
US-09-505-250-4  
; Sequence 4, Application US/09505250A  
; Patent No. 6329148  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Glenn  
; APPLICANT: Kao, Peter  
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with  
; TITLE OF INVENTION: Triptolides and Death Domain Ligands  
; FILE REFERENCE: SUN-109PRV2  
; CURRENT APPLICATION NUMBER: US/09/505,250A  
; CURRENT FILING DATE: 2000-02-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (153)...(854)  
US-09-505-250-4

Query Match 100.0%; Score 104; DB 4; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 7.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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Query Match      100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||
Db      2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||
Db      2868 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 8
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; TITLE: structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
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; DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match      100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||
Db      2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||
Db      2868 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 9
US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; FILE REFERENCE: 9855-3U1
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

Query Match      100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||
Db      2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||
Db      2868 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 10
US-09-341-587-7/c
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7
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Query Match 26.9%; Score 28; DB 4; Length 28720;  
Best Local Similarity 58.3%; Pred. No. 4.3;  
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 2 AATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGG 61  
Db 14762 AATTGAAGAGGTCCTTAGAGAGGAGAGGGGACATCTCCATTGTACCAAGTCTTCAGG 14703  
QY 62 AATCTGGAGACCAGGGAGCCTTTG 85  
Db 14702 TATTTGTGACAAGGAATCATCTG 14679

RESULT 11  
US-09-818-512-3  
; Sequence 3, Application US/09818512  
; Patent No. 6537780  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; FILE REFERENCE: C1001192  
; CURRENT APPLICATION NUMBER: US/09/818,512  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 116592  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(116592)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-818-512-3

Query Match 26.3%; Score 27.4; DB 4; Length 116592;  
Best Local Similarity 54.5%; Pred. No. 11;  
Matches 55; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
QY 4 TTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAA 63  
Db 81506 TCCAAACTATTGCCAGTAGCTTTCTGTTTCCCATCATTTTCAACCCAGAAATATTAT 81565  
QY 64 TCTGGAGACCAGGAGCCTTTGTTCTGGCCAGAAATGCTGC 104  
Db 81566 TTTCTTCCAGGAGGCATTAGCAGTACCTGGAAGCTCC 81606

RESULT 12  
US-09-169-768-1  
; Sequence 1, Application US/09169768  
; Patent No. 6492508  
; GENERAL INFORMATION:  
; APPLICANT: GRUSKIN, ELLIOT A.  
; APPLICANT: BUECHTER, DOUGLAS  
; APPLICANT: BROKAW, JANE  
; APPLICANT: ZHANG, GUANGHUI  
; APPLICANT: PAOLELLA, DAVID  
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DILWORTH & BARRESE  
; STREET: 333 EARLE OVINGTON BOULEVARD  
; CITY: UNIONDALE  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 11553  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,768  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEN, JEFFREY S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 228-8484  
TELEFAX: (516) 228-8516  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-169-768-1

Query Match 25.4%; Score 26.4; DB 4; Length 3170;  
Best Local Similarity 57.1%; Pred. No. 7.7;  
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTG 67  
Db 1307 AGCGAGGTGTTCCCGACCCCTGGCGCTGTCGGTCTCTGCTGGCAAGATGGAGAGGCTG 1366  
QY 68 GAGACCAGGAGGCCTTTGTTCTG 91  
Db 1367 GAGCTCAGGAGCCCTGGCCCTG 1390

RESULT 13  
US-09-169-768-15  
; Sequence 15, Application US/09169768  
; Patent No. 6492508  
; GENERAL INFORMATION:  
; APPLICANT: GRUSKIN, ELLIOT A.  
; APPLICANT: BUECHTER, DOUGLAS  
; APPLICANT: BROKAW, JANE  
; APPLICANT: ZHANG, GUANGHUI  
; APPLICANT: PAOLELLA, DAVID  
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DILWORTH & BARRESE  
; STREET: 333 EARLE OVINGTON BOULEVARD  
; CITY: UNIONDALE  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 11553  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/169,768  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEEN, JEFFREY S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 228-8484  
; TELEFAX: (516) 228-8516  
; INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3171 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-169-768-15

Query Match 25.4%; Score 26.4; DB 4; Length 3171;  
Best Local Similarity 57.1%; Pred. No. 7.7;  
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTG 67  
Db 1307 AGCGAGGTGTTCCCGGACCCCTGGCGCTGTGCGTCTGCTGGCAAAGATGGAGAGGCTG 1366  
QY 68 GAGACCAGGGAGCCCTTTGGTTCTG 91  
Db 1367 GAGCTCAGGGACCCCTGGCCCTG 1390

RESULT 14  
US-08-655-086-1  
; Sequence 1, Application US/08655086  
; Patent No. 5821089  
; GENERAL INFORMATION:  
; APPLICANT: GRUSKIN, ELLIOTT A.  
; APPLICANT: BUECHTER, DOUGLAS  
; APPLICANT: ZHANG, GUANGHUI  
; APPLICANT: CONNOLLY, KEVIN  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DILWORTH & BARRESE  
; STREET: 333 EARLE OVERTON BOULEVARD  
; CITY: UNIONDALE  
; STATE: NY  
; COUNTRY: US  
; ZIP: 11553  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/655,086  
; FILING DATE: 03-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEEN, JEFFREY S.  
; REGISTRATION NUMBER: 32,063  
; REFERENCE/DOCKET NUMBER: 203-1632  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-228-8484  
; TELEFAX: 516-228-8516  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3181 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
US-08-655-086-1

Query Match 25.4%; Score 26.4; DB 1; Length 3181;  
Best Local Similarity 57.1%; Pred. No. 7.7;  
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTG 67  
Db 1317 AGCGAGGTGTTCCCGGACCCCTGGCGCTGTGCGTCTGCTGGCAAAGATGGAGAGGCTG 1376  
QY 68 GAGACCAGGGAGCCCTTTGGTTCTG 91  
Db 1377 GAGCTCAGGGACCCCTGGCCCTG 1400

RESULT 15  
US-09-169-768-13  
; Sequence 13, Application US/09169768  
; Patent No. 6492508

GENERAL INFORMATION:  
; APPLICANT: GRUSKIN, ELLIOTT A.  
; APPLICANT: BUECHTER, DOUGLAS  
; APPLICANT: BROKAW, JANE  
; APPLICANT: ZHANG, GUANGHUI  
; APPLICANT: PAOLELLA, DAVID  
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DILWORTH & BARRESE  
; STREET: 333 EARLE OVERTON BOULEVARD  
; CITY: UNIONDALE  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 11553  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/169,768  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEEN, JEFFREY S.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 228-8484  
; TELEFAX: (516) 228-8516  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3349 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-169-768-13  
Query Match 25.4%; Score 26.4; DB 4; Length 3349;  
Best Local Similarity 57.1%; Pred. No. 7.9;  
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTG 67  
Db 1326 AGCGAGGTGTTCCCGGACCCCTGGCGCTGTGCGTCTGCTGGCAAAGATGGAGAGGCTG 1385  
QY 68 GAGACCAGGGAGCCCTTTGGTTCTG 91  
Db 1386 GAGCTCAGGGACCCCTGGCCCTG 1409  
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Job time : 85.6531 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 05:14:03 ; Search time 1850.07 Seconds  
(without alignments)  
207.072 Million cell updates/sec

Title: US-09-801-371A-1  
Perfect score: 104  
Sequence: 1 gaattcaactgggctcc.....ggtctggcagaatgctgc 104

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	104	100.0	104	US-09-801-371A-5	Sequence 5, Appli
3	104	100.0	1643	US-10-310-793-9	Sequence 9, Appli
4	104	100.0	1643	US-10-272-411-4	Sequence 4, Appli
5	104	100.0	1643	US-10-218-547-3	Sequence 3, Appli
6	104	100.0	1643	US-10-272-328A-4	Sequence 4, Appli
7	104	100.0	1666	US-10-247-671-68	Sequence 68, Appli
8	104	100.0	3634	US-09-824-322B-1	Sequence 1, Appli
9	104	100.0	3634	US-09-932-300-34	Sequence 34, Appli
10	104	100.0	3634	US-10-191-997-104	Sequence 104, App
11	104	100.0	4830	US-10-429-802-33	Sequence 33, Appli
12	104	100.0	4830	US-10-430-503-24	Sequence 24, Appli
13	93	89.4	1279	US-10-247-671-120	Sequence 120, App
14	77	74.0	81	US-09-801-371A-7	Sequence 7, Appli
15	59.8	57.5	3673778	US-10-312-841-1	Sequence 1, Appli

C	16	59.2	56.0	3673778	13	US-10-312-841-2	Sequence 2, Appli
	17	50	48.1	50	10	US-09-801-371A-8	Sequence 8, Appli
	18	43	41.3	43	10	US-09-801-371A-2	Sequence 2, Appli
C	19	43	41.3	43	10	US-09-801-371A-6	Sequence 6, Appli
	20	42	40.4	418	10	US-09-796-692-6223	Sequence 6223, Ap
	21	42	40.4	418	12	US-10-057-475B-6223	Sequence 6223, Ap
	22	42	40.4	418	12	US-10-154-884B-6223	Sequence 6223, Ap
	23	42	40.4	418	15	US-10-040-862-6223	Sequence 6223, Ap
	24	33	31.7	51	10	US-09-801-371A-10	Sequence 10, Appli
C	25	31	29.8	418550	12	US-10-292-798-1463	Sequence 1463, Ap
	26	30.4	29.2	440	12	US-10-062-674-37	Sequence 37, Appli
	27	30.2	29.0	45855	12	US-10-085-117-316	Sequence 316, App
C	28	29.2	28.1	2643	12	US-10-108-260A-754	Sequence 754, App
	29	28.8	27.7	1223197	13	US-10-027-632-179264	Sequence 179264,
C	30	28.8	27.7	1223197	14	US-10-027-632-179264	Sequence 179264,
	31	27.6	26.5	232	12	US-10-242-535A-46829	Sequence 46829, A
C	32	27.4	26.3	3617	9	US-09-874-069-2	Sequence 2, Appli
	33	27.4	26.3	116592	10	US-09-818-512-3	Sequence 3, Appli
	34	27.4	26.3	116592	13	US-10-354-065-3	Sequence 3, Appli
C	35	27.2	26.2	494	13	US-10-027-632-280709	Sequence 280709,
C	36	27.2	26.2	494	14	US-10-027-632-280709	Sequence 280709,
C	37	27.2	26.2	1392	15	US-10-156-761-524	Sequence 524, App
	38	27.2	26.2	45000	15	US-10-000-213-12	Sequence 12, Appli
	39	27.2	26.2	122186	11	US-09-563-728A-36	Sequence 36, Appli
C	40	27.2	26.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	41	27	26.0	860	13	US-10-027-632-8841	Sequence 8841, Ap
C	42	27	26.0	860	14	US-10-027-632-8841	Sequence 8841, Ap
	43	27	26.0	2895	12	US-10-159-563-71	Sequence 71, Appli
	44	27	26.0	2895	13	US-10-133-937-71	Sequence 71, Appli
	45	27	26.0	2915	13	US-10-354-358-43	Sequence 43, Appli

ALIGNMENTS

RESULT 1  
US-09-801-371A-1  
; Sequence 1, Application US/09801371A  
; Patent No. US20020155569A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaempfer, Raymond  
; APPLICANT: Osman, Farhat  
; APPLICANT: Jarroub, Nayef  
; APPLICANT: Ben-Asouli, Yitzhak  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH  
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES  
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147  
; CURRENT APPLICATION NUMBER: US/09/801,371A  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT WO 00/14255  
; PRIOR FILING DATE: 1999-09-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 104  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-801-371A-1

Query Match 100.0%; Score 104; DB 10; Length 104;  
Best Local Similarity 100.0%; Pred. No. 6.3e-28;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG	60
Db	1	GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG	60
QY	61	GAATCTGGAGACCAAGGAGCGCTTTGGTTCTTGGCCAGAAATGCTGC	104
Db	61	GAATCTGGAGACCAAGGAGCGCTTTGGTTCTTGGCCAGAAATGCTGC	104

RESULT 2



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US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

Query Match      100.0%; Score 104; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
Db 104 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 45

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 44 GAATCTGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1

RESULT 3
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PFS73
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-310-793-9

Query Match      100.0%; Score 104; DB 13; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1130 GAATCTGGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1173

RESULT 4
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
Db 1070 GAATTCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
Db 1130 GAATCTGGAGACACGAGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1173

RESULT 5
```

US-10-218-547-3  
; Sequence 3, Application US/10218547  
; Publication No. US20030100074A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel  
; TITLE OF INVENTION: Human Endokine Alpha  
; FILE REFERENCE: PF561  
; CURRENT APPLICATION NUMBER: US/10/218,547  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: 60/312,542  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 60/330,761  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: human  
US-10-218-547-3

Query Match 100.0%; Score 104; DB 15; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 1130 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 6  
US-10-272-328A-4  
; Sequence 4, Application US/10272328A  
; Publication No. US20030109444A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0206  
; CURRENT APPLICATION NUMBER: US/10/272,328A  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-272-328A-4

Query Match 100.0%; Score 104; DB 15; Length 1643;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 1130 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 7  
US-10-247-671-68

; Sequence 68, Application US/10247671  
; Publication No. US20030194721A1  
; GENERAL INFORMATION:  
; APPLICANT: Mikita, Thomas  
; APPLICANT: Shiffman, Dov  
; APPLICANT: Porter, Gordon, J.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
; FILE REFERENCE: PA-0050 US  
; CURRENT APPLICATION NUMBER: US/10/247,671  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/323,784  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PERL Program  
; SEQ ID NO 68  
; LENGTH: 1666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030194721A1 223092.1  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 1347, 1358  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-247-671-68

Query Match 100.0%; Score 104; DB 13; Length 1666;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60  
Db 1085 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1144  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 1145 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1188

RESULT 8  
US-09-824-322B-1  
; Sequence 1, Application US/09824322B  
; Publication No. US20030022848A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-AL  
; TITLE OF INVENTION: ALPHA EXPRESSION  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 1  
; LENGTH: 3634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)  
; NAME/KEY: exon  
; LOCATION: (615)..(981)  
; NAME/KEY: intron  
; LOCATION: (982)..(1588)  
; NAME/KEY: exon  
; LOCATION: (1589)..(1634)

/ NAME/KEY: intron  
/ LOCATION: (1635)..(1821)  
/ NAME/KEY: exon  
/ LOCATION: (1822)..(1869)  
/ NAME/KEY: intron  
/ LOCATION: (1870)..(2070)  
/ NAME/KEY: exon  
/ LOCATION: (2171)..(3381)  
/ PUBLICATION INFORMATION:  
/ AUTHORS: Nedwin, G.E.  
/ AUTHORS: Naylor, S.L.  
/ AUTHORS: Sakaguchi, A.Y.  
/ AUTHORS: Smith, D.  
/ AUTHORS: Jarrett-Nedwin, J.  
/ AUTHORS: Pennica, D.  
/ AUTHORS: Goeddel, D.V.  
/ AUTHORS: Gray, P.W.  
/ TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and  
/ TITLE: chromosomal localization  
/ JOURNAL: Nucleic Acids Res.  
/ VOLUME: 13  
/ ISSUE: 17  
/ PAGES: 6361-6373  
/ DATE: 1985-09-11  
/ DATABASE ACCESSION NUMBER: X02910 Genbank  
/ DATABASE ENTRY DATE: 1997-02-17  
US-09-824-322B-1

Query Match 100.0%; Score 104; DB 11; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 2808 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104  
Db 2868 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 9  
US-09-932-300-34  
; Sequence 34, Application US/09932300  
; Publication No. US20030032788A1  
; GENERAL INFORMATION:  
; APPLICANT: GARVER, Eric  
; APPLICANT: TU, Guang-Chou  
; APPLICANT: ISRAEL, Yedy  
; TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION  
; FILE REFERENCE: 9855-3U2  
; CURRENT APPLICATION NUMBER: US/09/932,300  
; CURRENT FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: US 60/051,705  
; PRIOR FILING DATE: 1997-07-03  
; PRIOR APPLICATION NUMBER: US 09/109,663  
; PRIOR FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 3634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-932-300-34

Query Match 100.0%; Score 104; DB 11; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 2808 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104  
Db 2868 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 10  
US-10-191-997-104  
; Sequence 104, Application US/10191997  
; Publication No. US20030207834A1  
; GENERAL INFORMATION:  
; APPLICANT: Oligos Etc., Inc.  
; APPLICANT: DALE, Roderic M. K.  
; APPLICANT: ARROW, Amy  
; APPLICANT: THOMPSON, Terry  
; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Thei  
; FILE REFERENCE: 54800-5019  
; CURRENT APPLICATION NUMBER: US/10/191,997  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,820  
; PRIOR FILING DATE: 2001-07-10  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 104  
; LENGTH: 3634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: X02910  
US-10-191-997-104

Query Match 100.0%; Score 104; DB 13; Length 3634;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 2808 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104  
Db 2868 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 11  
US-10-429-802-33  
; Sequence 33, Application US/10429802  
; Publication No. US20030228285A1  
; GENERAL INFORMATION:  
; APPLICANT: HUNG, MIEN-CHIE  
; APPLICANT: WONG, KA YIN  
; APPLICANT: ZOU, YIYU  
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER  
; FILE REFERENCE: UTSC:752US  
; CURRENT APPLICATION NUMBER: US/10/429,802  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: 60/377,672  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 4830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-429-802-33

Query Match 100.0%; Score 104; DB 12; Length 4830;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 2781 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 2840

QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 2841 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2884

RESULT 12  
US-10-430-503-24  
; Sequence 24, Application US/10430503  
; Publication No. US20040005684A1  
; GENERAL INFORMATION:  
; APPLICANT: HUNG, MIEN-CHIE  
; APPLICANT: LAN, KENG-LI  
; APPLICANT: OU-YANG, FU  
; APPLICANT: LIU, JAW-CHING  
; APPLICANT: LAN, KENG-HSIN  
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: UTSC:797US  
; CURRENT APPLICATION NUMBER: US/10/430,503  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: 60/383,063  
; PRIOR FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 4830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-430-503-24

Query Match 100.0%; Score 104; DB 12; Length 4830;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCTCCAGAACTCACTGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 2781 GAATTCAAACTGGGCTCCAGAACTCACTGGGCTTACAGCTTTGATCCCTGACATCTG 2840  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 2841 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2884

RESULT 13  
US-10-247-671-120  
; Sequence 120, Application US/10247671  
; Publication No. US20030194721A1  
; GENERAL INFORMATION:  
; APPLICANT: Mikita, Thomas  
; APPLICANT: Shiffman, Dov  
; APPLICANT: Porter, Gordon, J.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS  
; FILE REFERENCE: PA-0050 US  
; CURRENT APPLICATION NUMBER: US/10/247,671  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/323,784  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PERL Program  
; SEQ ID NO 120  
; LENGTH: 1279  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1  
US-10-247-671-120

Query Match 89.4%; Score 93; DB 13; Length 1279;  
Best Local Similarity 99.0%; Pred. No. 9.5e-24;  
Matches 104; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GAATTCAAACTGGGCTCCAGAACTCACTGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 1077 GAATTCAAACTGGGCTCCAGAACTCACTGGGCTTACAGCTTTGATCCCTGACATCTG 1136  
QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104  
Db 1137 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1181

RESULT 14  
US-09-801-371A-7  
; Sequence 7, Application US/09801371A  
; Patent No. US20020155569A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaempfer, Raymond  
; APPLICANT: Osman, Farhat  
; APPLICANT: Jarrous, Nayef  
; APPLICANT: Ben-Asouli, Yitzhak  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH  
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES  
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147  
; CURRENT APPLICATION NUMBER: US/09/801,371A  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT WO 00/14255  
; PRIOR FILING DATE: 1999-09-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 81  
; TYPE: RNA  
; ORGANISM: Homo sapien  
US-09-801-371A-7

Query Match 74.0%; Score 77; DB 10; Length 81;  
Best Local Similarity 79.2%; Pred. No. 3.8e-18;  
Matches 61; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCTCCAGAACTCACTGGGCTTACAGCTTTGATCCCTGACATCTG 60  
Db 5 GAAUUCAAACUGGGCCUCCAGAACUCACUGGGCCUACAGCUUGAUCUCCUGACUUCUG 64  
QY 61 GAATCTGGAGACCAAGG 77  
Db 65 GAAUCUGGAGACCAAGG 81

RESULT 15  
US-10-312-841-1  
; Sequence 1, Application US/10312841  
; Publication No. US20030186277A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH  
; FILE REFERENCE: E01/1208/WO  
; CURRENT APPLICATION NUMBER: US/10/312,841  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 3673778  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; NAME/KEY: unsure  
; LOCATION: (3294164)  
US-10-312-841-1

Query Match 57.5%; Score 59.8; DB 13; Length 3673778;  
Best Local Similarity 73.8%; Pred. No. 4.1e-11;  
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;